

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 17, 2005, 00:47:35 ; Search time 40 Seconds  
(without alignments)  
894.816 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAAALITLVRSQGNVRRR.....KNSINFSRGSFASGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360	18.5	348	T50783	protein phosphatas
2	357	18.3	383	T48018	hypothetical prote
3	344.5	17.7	392	T84650	probable protein p
4	338	17.3	434	T04263	phosphoprotein pho
5	337.5	17.3	381	T09640	protein phosphatas
6	332.5	17.0	359	T52337	phosphoprotein pho
7	328	16.8	362	T84695	probable protein p
8	326	16.7	464	T896700	protein F12A21.5
9	325	16.7	281	T41854	phosphoprotein pho
10	322.5	16.5	239	T01361	probable protein p
11	322.5	16.5	816	T48123	hypothetical prote
12	322	16.5	511	T96752	protein phosphatas
13	321.5	16.5	347	T456058	phosphoprotein pho
14	320	16.4	355	T84643	probable protein p
15	319.5	16.4	389	T05095	hypothetical prote
16	319.5	16.4	390	T820392	phosphoprotein pho
17	319.5	16.4	397	TJ2524	phosphoprotein pho
18	318.5	16.3	423	T48121	hypothetical prote
19	318	16.3	238	T96811	hypothetical prote
20	311.5	16.0	361	T45778	protein phosphatas
21	310.5	15.9	383	T38772	protein phosphatas
22	307.5	15.8	382	T82423	phosphoprotein pho
23	307.5	15.8	390	T45602	phosphoprotein pho
24	307.5	15.8	393	T49016	phosphoprotein pho
25	307.5	15.8	396	T02483	probable protein p
26	306.5	15.7	382	T52422	phosphoprotein pho
27	306.5	15.7	382	T53823	magnesium dependen
28	306.5	15.7	382	T32399	phosphoprotein pho
29	306.5	15.7	414	T82462	protein phosphatas

30	305	15.6	370	2	S54297	protein phosphatas
31	304	15.6	404	2	T00750	probable protein p
32	304	15.6	442	2	B86209	protein F2205.22
33	301	15.4	357	2	T06308	protein phosphatas
34	301	15.4	1428	2	T13926	probable protein p
35	300.5	15.4	300	2	A55804	phosphoprotein pho
36	288.5	14.8	268	2	T04610	protein phosphatas
37	288	14.8	281	2	F86355	T16E15.10 protein
38	287.5	14.7	242	2	T18588	probable protein p
39	285.5	14.6	290	2	E84591	probable protein p
40	285.5	14.6	380	2	E84748	probable protein p
41	281	14.4	399	2	S55457	phosphoprotein pho
42	279	14.3	406	2	A47492	phosphoprotein pho
43	278.5	14.3	405	2	F86206	hypothetical prote
44	278.5	14.3	514	2	D84584	probable protein p
45	278	14.2	348	2	E88434	protein T23F11.1

ALIGNMENTS

RESULT 1

T50783

protein phosphatase 2C-like protein - Arabidopsis thaliana

N;Alternate names: protein T30N20\_10

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004

C;Accession: T50783

R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Mew

submitted to the Protein Sequence Database, July 2000

A;Reference number: Z25240

A;Accession: T50783

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-348 <BEV>

A;Cross-references: UNIPROT:Q9LEW5; EMBL:AL365234

A;Experimental source: cultivar Columbia; BAC clone T30N20

C;Genetics:

A;Map position: 5

A;Introns: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3

A;Note: T30N20\_10

C;Superfamily: human phosphoprotein phosphatase 1A

Query Match	18.5%	Score 360;	DB 2;	Length 348;
Best Local Similarity	35.4%	Pred. No. 1.3e-22;		
Matches	99;	Conservative	56;	Mismatches 89;
				Indels 36;
				Gaps 11;
Qy	96	GCASQIGRKKEKEDRFD--FAQLTDEVL-YFAYVDHGGGAADFCFTHHEKICIMDLPLK	152	
Db	35	GYASSAGKRSMEDFPETRIDGINGEIVGLFVFDHGGGARAAYVKRHL---FSLNLI	91	
Qy	153	EK---NLETLTLTFLAFLDID---KAFSSHARLSADATLLTSGTTATVALLRDGIELVVAS	205	
Db	92	PKFISDTSKAITDAYNHTDSELLKSENHR-----DAGSTASTAIL-VGRLVVAN	142	
Qy	206	VGDSRAILCKGPKMLTIDHTPERKDEKERIKCGFVAVNSLQGFVNGRLAMTRSIG	265	
Db	143	VGDSRAVISGGKAIAVSRDHKPDQSDERIERIENAGGFVWM-----AGVLAVSRAFG	194	
Qy	266	DLDLKTSGVIAEPETKRIKULHADDSS--FLVLTDTGTFNFMVNSQEIFCFVNCQHDPEAA	323	
Db	195	DRLLK-QYVVADPEIQEKI---DDTLEFLILASDGLWDVFSNEAAVAVMKEVEDPEDSA	250	
Qy	324	HAVTEQAIQGTEDNSTAVVVPFGAWGKYKNSEINFESR	363	
Db	251	KKLVGGAIKRGSADNITCVVVVRFLEKKSASSSHISSSSK	290	

RESULT 2

T48018

hypothetical protein T1J713.220 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

Qy 302 FMVNSQLICFVQ-----CHDPN-----EAAHATEQAIQVG 334

Db 351 DVMTDEEACEAMARKILLWHKKNVAGDASLLADRRKEGKDPAAWSAAEYLSKLAIQRG 410

Db	22	CSQLDINTPD-----AVSDNSLASTMLOFVNIRSGS-----FADIG	58
Qy	103	KRXENED---RFD-----FAQLTDEVLYFAYVDGHHGSPAADFCHTHMEKICMD--L	149
Db	59	PRXYMEDEHIRIDDLVSQLGSLFRCPKPSAFYGVDFDGGSEAAAYRVENVMRPFEDVS	118
Qy	150	LPKEKUL-----ETLLTLAFLEIDKAPSSHARLSADATLLTSGTTATVALLRDGTEL	201
Db	119	FPEASELDEIFLEGVENCLERRAPFLADLALADCCSIST-----SSGTALTALVL-GRUL	172
Qy	202	VWASVGDRAILCRKGPKMLTTIDHTPERKDEKERIKCGGFVAMWSLQGPHVNGRLAMT	261
Db	173	LVNAGDCRAVLCKRGEAIDMSQDHRITYSEKERVBELGYV-----DDGYINGVLSVS	227
Qy	262	RSIGDLDLK-----TSGVIAPEPTKRIKLHHADDSFLVLTDTGDNFMVNSQBCDFV---	313
Db	228	RALGDWDMKLPKGSASPLISEPELRQILTE-DDEFLIIGCDGIWDVSISSQQAQSVIRWG	286
Qy	314	-NOCHDPNEAAHATEQAIQYGTEDNSTAVVVPFGA	348
Db	287	LKHHDDPEQSAKDOLVNEALRRHTIDNLTVIIVCFSS	322

RESULT 7

F84695

probable protein phosphatase 2C [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C/Accession: F84695

C/Link, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanNaken, S.E.; Umayam, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: F84695

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-362 <STO>

A/Cross-references: UNIPROT:Q9ZW21; GB:AE002093; NID:g3980397; PIDN:AAC95200.1

C/Genetics:

A/Gene: At2g29380

A/Map position: 2

C/Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220

18	RRRVLLSSRLIQDORRVTPTCHSTSTSPRCRFRPDGSGSP-ATWDFGIMWNRIDEPI	76
26	RRRPRFQVHMEDWEK--NCKRSKQEAALATRY---SSIPRSSREDFS--QDNVD---	72
77	LPPIKYGKPIPKISLENVCASOIGKRKENED-----RPFDAQLTDEVLVYA	124
73	-----VSSPRYGVSSVCGRRREMEDAVAIHPFSPPKNSFPFQ-----HYFG	114
125	VDYDGHGGPAAADFCHTHMEKIMDLLPK----EKNELTLLTLAPLEIDK-----AFS	172
115	VDYDGHGSHVAARCRERLHKVLQBELSSDMEDEEWKTTMERSFTFMDKEVSWGDSVVT	174
173	SHARLSADATLLTTS-GTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERK	231
175	ANCKCDLQTPACDSVGSTAVSVITPD-KIVVANGCDSRAVLCRNGKPVPLSTDHKPDPR	233
232	DEKERIKKCG-FVAMNSLGOPHYNGRIAMWTRTSIGDLTKTSGVTAABE---TKRIKLHH	287
234	DELDRIEGAGGRVITYWDC---PVLGVGLAMSGRAIGDNLKPY-VSCEPEVITIDR-----	284
288	ADDSFLVLTTDGINFMVNSQELCFVNQC-----HDP-----NEAAHAHVTEOA	330
285	RDDCLLTASGLMDVWVNETACSVARMCLRGGRRRQDNEDPAISDKATCWASVLTKULA	344

QY 331 IQYGTEDNSTAVV 344  
: : : : :  
Db 345 LARNSSDNVSVV 358

RESULT 8

H96700  
protein F12A21.5 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: H96700  
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;  
ansen, N.F.; Hughes, B.; Huizlar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: H96700  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-464 <STO>  
A;Cross-references: UNIPROT:Q9FXE4; GB:AB005173; NID:g11072032; PIDN:AAG28911.1; GSPDB:G  
C;Genetics:  
A;Gene: F12A21.5  
A;Map position: 1

Query Match 16.7%; Score 326; DB 2; Length 464;  
Best Local Similarity 31.2%; Pred. No. 1.4e-19;  
Matches 99; Conservative 47; Mismatches 107; Indels 64; Gaps 11;

QY 96 GCASQIGKKEKEDRDFDAQL---TDEVLVYFVYDGGGPAADFCFTHMEKICIMDLP- 151  
Db 122 GVVSRRGKKKFMEDTHRIVPCLVGNKSGGFFGYDGGGAKAAEFVAENLHKYVEMMEN 181  
QY 152 ---KENKLETLTLAFLAIDKAFSSHARLSADATLTSGTATVALLRDGLVWASVGD 208  
Db 182 CKGKEKVEA-FRAAFRTDRDLEFKVKEQSLKGVVSGACCTAVIQDQ-EMIVNLGD 239  
QY 209 SRALCRKGKPKMLTIDHTPERKDEKERIKK-----CGGFVAMNSLQPHVNGR 257  
Db 240 CRAVLCRAGVAEALTDHKGPRDDEKIERIESQSLIPFMTFGLQGYVD-NHOGAMRVQGI 298  
QY 258 LAMTRSIGDLTKTSVIAEPETKRIKLHADDPSFLVLTDDGINFVNSOE----- 308  
Db 299 LAVRSIGDAHLK-KWVAEPETRVLEBQ-DMEFLVLASDGLVDVNSQEAQVYTVLHVL 356  
QY 309 -----ICDFVNOCHDPN-----EAAHVAVTEQAIQYGTEDNSTAVVFPFG 347  
Db 357 AQRKTPKESEENLVQGFVNMSPSSKLRLASLVKSPCAKQSYNNSESPSL----- 411  
QY 348 AWGKYKNSEINFSPRS 364  
Db 412 -----NREIGSSPSKS 422

RESULT 9

S41854  
phosphoprotein phosphatase (EC 3.1.3.16) PTC1 - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein D2925; protein serine/threonine phosphatase; protein YD8119.0  
C;Species: Saccharomyces cerevisiae  
C;Date: 31-Mar-1992 #sequence\_revision 14-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S41854; S52513; S50976; S67538  
R;Maeda, T.; Tsai, A.Y.M.; Saito, H.  
Mol. Cell. Biol. 13, 5408-5417, 1993  
A;Title: Mutations in a protein tyrosine phosphatase gene (PTP2) and a protein serine/th  
A;Reference number: S41854; MUID:93360976; PMID:8395005  
A;Accession: S41854

A;Molecule type: DNA  
A;Residues: 1-281 <MAE>  
A;Cross-references: UNIPROT:P35182; EMBL:L14593; NID:g402502; PIDN:AAA34920.1; PID:g40250  
R;Andre, B.; Visser, S.; Urrestazu, L.  
submitted to the EMBL Data Library, February 1995  
A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV f  
A;Reference number: S52492  
A;Accession: S52513  
A;Molecule type: DNA  
A;Residues: 1-281 <AND>  
A;Cross-references: EMBL:Z48432; NID:g683669; PID:g683691  
R;Murphy, L.; Richards, C.; Gentles, S.; Harris, D.  
submitted to the EMBL Data Library, January 1995  
A;Reference number: S50976  
A;Accession: S50976  
A;Molecule type: DNA  
A;Residues: 167-281 <MUR>  
A;Cross-references: EMBL:Z48008; NID:g642799; PID:g642800  
R;Urrestazu, L.A.; Andre, B.; Visser, S.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67538  
A;Accession: S67538  
A;Molecule type: DNA  
A;Residues: 1-281 <URR>  
A;Cross-references: EMBL:Z74054; NID:g1430964; PID:e253189; PID:g1430965; MIPS:YDL006W  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:PTC1  
A;Cross-references: SGD:S0002164; MIPS:YDL006W  
A;Map position: 4L  
C;Keywords: phosphoric monoester hydrolase

Query Match 16.7%; Score 325; DB 2; Length 281;  
Best Local Similarity 32.8%; Pred. No. 8.7e-20;  
Matches 79; Conservative 48; Mismatches 82; Indels 32; Gaps 7;  
QY 122 YFAYDGGGPAADFCFTHMEKICIND--LLPKKLETLTLAFLAIDKAFSSHARLSA 179  
Db 53 YFAYDGGGPAADFCFTHMEKICIND--LLPKKLETLTLAFLAIDKAFSSHARLSA 179  
QY 180 DATLTSGTATVALLR-----DGI-----ELVVASVGDRAILCRKGKPKMLT 223  
Db 107 -KLGVNSGCTTAAVCVLRWELPDSVSDSDMLAQHQRKLYTANVGDRIVLFNNGSIRLT 165  
QY 224 IDHTPERKDEKERIKKCGGFVAMNSLQPHVNGRLAMTRSIGDLTKTSVIAEPETKRI 283  
Db 166 YDHKASDTLEMQRVEQAQGLIM-----KSRVNGMLAVTRSLGD-KPFDSLVVSGSPFTTSV 219  
QY 284 KLHADDPSFLVLTDDGINFVNSOEICDFVNOCHDPNEAAHVAVTEQAIQYGTEDNSTAVV 343  
Db 220 EI-TSEDKFLILACDGLVDVDDQDACELIKDITPEPNAKVLRYALENGTTDNTVMV 278  
QY 344 V 344  
Db 279 V 279

RESULT 10

T01361  
probable protein phosphatase 2C At2g34740 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: T01361; D84760  
R;Rounsley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,  
submitted to the EMBL Data Library, May 1998  
A;Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.  
A;Reference number: Z14179  
A;Accession: T01361  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-239 <ROU>  
A;Cross-references: UNIPROT:O64583; EMBL:AC003096; NID:g3132469; PID:g3132471  
A;Experimental source: cultivar Columbia



A:Molecule type: DNA  
A:Residues: 1-355 <STO>  
A/Cross-references: UNIPROT:081716; GB:AE002093; NID:g4559345; PIDN:AAD23006.1; GSPDB:GM  
C:Genetics:  
A:Gene: At2g25070  
A:Map position: 2  
C:Superfamily: human phosphoprotein phosphatase 1A

	Query Match	16.4%; Score 320;	DB 2;	Length 355;
	Best Local Similarity	30.8%; Pred. No. 3.1e-19;	Mismatches 44;	Indels 68; Gaps 9;
	Matches	96;	Conservative	104;
Qy	96 GCASQIGKRKENED-RDFAQLTDEVLYFAYVDGHHGGPAAADFCHTHM-EKICMDLLPK 153	:	:	:
Dd	25 GLSSQGWRATMEDAHAILDLDDKTSGFGVYDGHGKVAKFCARYLHQOVISNEYKT 84	:	:	:
Qy	154 KNLFTLTALPLETD-----KAFSSHARLS----- 178	:	:	:
Dd	85 GDVETSLRRAPFRDMQMGGQRWRELVLGDKNKMGSMIEGFIWSPRSGDTNNQPDWS 144	:	:	:
Qy	179 -----ADATLLTSGTTATVALLRDGIELVASVGDSRAILCRKGPKMLTIIDHTPERK 231	:	:	:
Dd	145 PLEDGPHSDFTGPTSGCTACVALIKDK-KLFVANAGDSRCVISRSQAYNLSKDHPDLE 203	:	:	:
Qy	232 DEKERIKKCGGFVAWNLSGQPHVNGRLAMTRSIGOLDLTKTSG-----VIAPEPTKRI 283	:	:	:
Dd	204 VEKERILKAGGFI-----HAGRINGSLLNLAIGDMFEFKNQKFLPSEKQMVTA DPDI NTI 258	:	:	:
Qy	284 KLHHADSFLVLTWDGINFMVNSOEICDFVNQCNDPNEAAHAHVTRQAIQYGTE----- 336	:	:	:
Dd	259 DLCD-DDDFLVVACDGIWDCMSQELVDPIHEQLKSETKLSTVCEKVVDRCLAPDTATGE 317	:	:	:
Qy	337 --DNSTAVVVPF 346	:	:	:
Dd	318 GCDNMVTILLVQP 329	:	:	:

RESULT 15  
T05095  
hypothetical protein F28M20.60 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T05095  
R:Bavan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, I.  
submitted to the Protein Sequence Database, November 1998  
A:Reference number: Z15398  
A:Accession: T05095  
A:Molecule type: DNA  
A:Residues: 1-389 <BEV>  
A/Cross-references: UNIPROT:081773; EMBL:AL0311004  
A:Experimental source: cultivar Columbia; BAC clone F28M20  
C:Genetics:  
A:Map position: 4  
A:Introns: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3  
A>Note: F28M20.60  
C:Superfamily: human phosphoprotein phosphatase 1A

	Query Match	16.4%; Score 319.5;	DB 2;	Length 389;
	Best Local Similarity	30.8%; Pred. No. 3.9e-19;	Mismatches 45;	Indels 81; Gaps 11;
	Matches	97;	Conservative	92;
Qy	96 GCASQIGKRKENED----RFPDPAQLTDEVLYFAYVDGHHGGPAAADFCHTHMEKCIMDLLP 151	:	:	:
Dd	60 GYASSPGKRSSMEDFYETRIGVE-GEIVGLFGVFDPGHGARAEEVKQNLI---FSNLIR 115	:	:	:
Qy	152 KEKNLETLLTLAPLEIDKAFSSHARLSADATLLTS-----GTTATVALLRDGIELV 203	:	:	:
Dd	116 HPK-----FISDTTAAIADAYNQTDSEPLKSSENSQNRDAGSTASTAIL-VGRDLLV 165	:	:	:
Qy	204 ASVGDSRAILCRKGPKMLTIIDHTPERKDEKRIKKCGFVAWNLSGQPHVNGRLAMTRS 263	:	:	:
Dd	166 ANVGDSRAVICRGNAITAVSRDHPRDQSDERKRIEDAGGVFWM--AGTWRVGVVLAVSRA 223	:	:	:

Qy	264	IGDLKTSVIAEPE-----TKRIKLHH-----	287
Db	224	FGRLK-QYVADPEIQVLTFCQNLLEYIKNATLLTIEHNLHWISIVSYLNGTLQNFL	282
Qy	288	-----ADDS--FLVLTDDGINFMVNSOEICDFVNOCHDPNEAAHAVTEQAI	331
Db	283	RSLISINGKFQEEKVDSLEFLILASDGLWDVVSNBEEAVGMKAIKIEDPEEGAKRLMMEAY	342
Qy	332	QYGTEDNSTAVVVPF	346
Db	343	QSGADNITCVRVF	357

Search completed: June 17, 2005, 00:57:51  
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: June 17, 2005, 00:39:24 ; Search time 171 Seconds  
(without alignments)  
1113.997 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSQGNVRR.....KNSINFSPSRFPASSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1951	100.0	372	2 Q8N3J5	Q8N3J5 homo sapien
2	1950	99.9	372	2 Q6EN45	Q6EN45 homo sapien
3	1945	99.7	372	2 Q8IUT7	Q8IUT7 homo sapien
4	1777	91.1	372	2 Q8BXN7	Q8BXN7 mus musculus
5	1399.5	71.7	373	2 Q6ING9	Q6ING9 xenopus lae
6	951.5	48.8	233	2 Q8IXG7	Q8IXG7 homo sapien
7	950	48.7	182	2 Q8ND70	Q8ND70 homo sapien
8	369	18.9	348	2 Q6TUX7	Q6TUX7 oryza sativ
9	369	18.9	354	2 Q8LAY8	Q8LAY8 arabidopsis
10	360	18.5	348	2 Q8LEW5	Q8LEW5 arabidopsis
11	358	18.3	290	2 Q6IV73	Q6IV73 zea mays (m
12	357	18.3	383	2 Q9MIP8	Q9MIP8 arabidopsis
13	354.5	18.2	352	2 Q653S3	Q653S3 oryza sativ
14	354.5	18.2	362	2 Q653S4	Q653S4 oryza sativ
15	354.5	18.2	423	1 P2C2 ARATH	Q04719 arabidopsis
16	352	18.0	282	2 Q7XR06	Q7XR06 oryza sativ
17	350.5	18.0	303	2 Q81OH0	Q81OH0 mus musculus
18	350.5	18.0	360	2 Q8BHN0	Q8BHN0 m mus muscu
19	350.5	18.0	360	2 Q8C021	Q8C021 m mus muscu
20	348	17.8	319	2 Q8S820	Q8S820 mesembryant
21	348	17.8	491	2 Q8L5C4	Q8L5C4 oryza sativ
22	346.5	17.8	388	2 Q8H610	Q8H610 oryza sativ
23	344.5	17.7	392	2 Q9SLA1	Q9SLA1 arabidopsis
24	344	17.6	311	2 Q8RXV3	Q8RXV3 arabidopsis
25	344	17.6	420	2 Q8VZD9	Q8VZD9 arabidopsis
26	342	17.5	394	2 Q84OD6	Q84OD6 nicotiana t
27	342	17.5	420	2 Q94AT1	Q94AT1 arabidopsis
28	340.5	17.5	280	2 Q9FYN7	Q9FYN7 oryza sativ
29	338.5	17.4	276	2 Q6FWM3	Q6FWM3 candida gla
30	338	17.3	434	1 P2C1 ARATH	P49597 arabidopsis
31	337.5	17.3	381	2 Q24078	Q24078 medicago sa

32	337	17.3	363	2 Q6EN45	Q6EN45 oryza sativ
33	335	17.2	243	2 Q8S3P1	Q8S3P1 oryza sativ
34	334.5	17.1	362	2 Q9ZPL9	Q9ZPL9 lotus japon
35	334.5	17.1	380	2 Q8S821	Q8S821 mesembryant
36	333.5	17.1	371	2 Q8VZN9	Q8VZN9 arabidopsis
37	333.5	17.1	387	2 Q6L5H6	Q6L5H6 oryza sativ
38	332.5	17.0	359	2 Q82469	Q82469 mesembryant
39	332	17.0	283	2 Q8L714	Q8L714 arabidopsis
40	332	17.0	445	2 Q6L4R7	Q6L4R7 oryza sativ
41	329	16.9	339	2 Q757M1	Q757M1 ashbya goss
42	328	16.8	362	2 Q9ZW21	Q9ZW21 arabidopsis
43	326	16.7	307	2 Q9FGM3	Q9FGM3 arabidopsis
44	326	16.7	464	2 Q9FXE4	Q9FXE4 arabidopsis
45	325	16.7	281	1 P2C1_YEAST	P35182 saccharomyc

## ALIGNMENTS

RESULT 1			
ID	Q8N3J5	PRELIMINARY;	PRT; 372 AA.
AC	Q8N3J5;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Hypothetical protein DKFzp761G058 (Protein phosphatase 2C kappa)		
DE	(PP2C-like protein).		
GN	Name=DKFzp761G058;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Amygdala;		
RG	The German cDNA Consortium;		
RA	Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,		
RA	Fobo G., Han M., Wiemann S.;		
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.		

Query Match 100.0%; Score 1951; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 4.5e-154; Indels 0; Gaps 0;  
Matches 372; Conservative 0; Mismatches 0;

QY 1 MSTAALITLVRSQGNVRRVRLSSRLLODRRVTPTCHSSTSEPRCSRFDPDGGSPAT 60

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Db      1 MSTAAITLVRSGNQVRRVLLSSRLQDDRRVPTCHSSSTSEPRCSRFPDGGSGPAT 60
QY      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120
Db      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120
QY      121 LYFVAVDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180
Db      121 LYFVAVDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180
QY      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKKC 240
Db      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKKC 240
QY      241 GGFVAVNSLQGPVNGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDLVLTDDGI 300
Db      241 GGFVAVNSLQGPVNGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDLVLTDDGI 300
QY      301 NFMVNSQECDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVVPFGANGKYKNSEINFS 360
Db      301 NFMVNSQECDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVVPFGANGKYKNSEINFS 360
QY      361 FSRSPASSGRWA 372
Db      361 FSRSPASSGRWA 372

RESULT 2
Q96NT4 ID Q96NT4 PRELIMINARY; PRT; 372 AA.
AC Q96NT4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein FLJ30116.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oabayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togliya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukutsumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA "Complete sequencing and characterization of 21,243 full-length human

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RT      CDNAS;
RL      Nat. Genet. 36:40-45(2004).
CC      -I- SIMILARITY: Belongs to the PP2C family.
DR      EMBL; AK054678; BAB70790.1; -.
DR      HSSP; P35813; 1A60.
DR      GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR      GO; GO:0016787; F:hydrolase activity; IEA.
DR      GO; GO:0000287; F:magnesium ion binding; IEA.
DR      GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR      GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR      InterPro; IPR000222; PP2C.
DR      InterPro; IPR001932; PP2C-like.
DR      Pfam; PF00481; PP2C; 1.
DR      SMART; SM00332; PP2C; 1.
DR      SMART; SM00331; PP2C-SIG; 1.
DR      PROSITE; PS01032; PP2C; 1.
KW      Hydrolase; Magnesium.
SQ      SEQUENCE 372 AA; 40983 MW; 7065B29DC79CB93B CRC64;

Query Match      99.9%; Score 1950; DB 2; Length 372;
Best Local Similarity 99.7%; Pred. No. 5.4e-154;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSTAAITLVRSGNQVRRVLLSSRLQDDRRVPTCHSSSTSEPRCSRFPDGGSGPAT 60
Db      1 MSTAAITLVRSGNQVRRVLLSSRLQDDRRVPTCHSSSTSEPRCSRFPDGGSGPAT 60

QY      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120
Db      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120

QY      121 LYFVAVDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180
Db      121 LYFVAVDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180

QY      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKKC 240
Db      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKKC 240

QY      241 GGFVAVNSLQGPVNGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDLVLTDDGI 300
Db      241 GGFVAVNSLQGPVNGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDLVLTDDGI 300

QY      301 NFMVNSQECDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVVPFGANGKYKNSEINFS 360
Db      301 NFMVNSQECDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVVPFGANGKYKNSEINFS 360

QY      361 FSRSPASSGRWA 372
Db      361 FSRSPASSGRWA 372

RESULT 3
Q8IUZ7 ID Q8IUZ7 PRELIMINARY; PRT; 372 AA.
AC Q8IUZ7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp761G058.
GN Name=DKFZp761G058;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Pituitary;  
RC TISSUE=Pituitary;  
RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Retina;  
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Carninci P., Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Retina;  
RC The FANTOM Consortium;  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Retina;  
RC MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Retina;  
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitasuna T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Retina;  
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Query Match 99.78; Score 1945; DB 2; Length 372;  
Best Local Similarity 99.78; Pred. No. 1.4e-153;  
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRFPDGGSGSPAT 60  
DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRFPDGGSGSPAT 60  
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCSAQIGRKENEDRFPALTDV 120  
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCSAQIGRKENEDRFPALTDV 120  
QY 121 LYFAVYDGHGGAADPCHTHMEKIMDLPLPKENKLETILTLPLETDKAFSSHARLSAD 180  
DB 121 LYFAVYDGHGGAADPCHTHMEKIMDLPLPKENKLETILTLPLETDKAFSSHARLSAD 180  
QY 181 ATLLTSGTTATVALLRDGIELVWASVGSRAILCRKGPWKLTIDHPERKDEKIRKCC 240  
DB 181 ATLLTSGTTATVALLRDGIELVWASVGSRAILCRKGPWKLTIDHPERKDEKIRKCC 240  
QY 241 GGFVAVNSLGGPHVNGRLAMTRISGDLDTKTSVGIVAPETKRIKLHADDSDFLVLTDDGI 300  
DB 241 GGFVAVNSLGGPHVNGRLAMTRISGDLDTKTSVGIVAPETKRIKLHADDSDFLVLTDDGI 300  
QY 301 NFVNSQIEICDFVNOCHDPPNEAAHVAETQAIOYGTEDNSTAVVPPGAGWKYKNSINFS 360  
DB 301 NFVNSQIEICDFVNOCHDPPNEAAHVAETQAIOYGTEDNSTAVVPPGAGWKYKNSINFS 360  
QY 361 FSRSFASGRWA 372  
DB 361 FSRSFASGRWA 372



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Db 300 GINFINVSGEIDIIHQCHDPKEAAQVTEQAIOYGTEDNSTAIVVFPFGAWGKHKSSEVS 359
QY 359 FFSRSFASGRW 371
Db 360 FFSRGSFASGRW 372

RESULT 6
ID Q8IXG7 PRELIMINARY; PRT; 233 AA.
AC Q8IXG7;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE U0882E07.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MAO Y., Xie Y.;
RA Submited (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PP2C family.
EMBL: AF351614; AA76514.1; -.
DR GO: 0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO: 0016787; F:hydrolase activity; IEA.
DR GO: 0000287; F:magnesium ion binding; IEA.
DR GO: 0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO: 0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR000222; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 233 AA; 25692 MW; EB90A7B3BC1BDD08 CRC64;

Query Match 48.8%; Score 951.5; DB 2; Length 233;
Best Local Similarity 86.6%; Pred. No. 5e-71;
Matches 187; Conservative 5; Mismatches 17; Indels 7; Gaps 1;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCHTHMEKICMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKICMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
QY 181 ATLLTSGT-----TATVLRDGIWVAVSGDS 209
Db 181 ENCAWAAALDLEPVDTCGASVEREICLLISQVKS 216

RESULT 7
ID Q8ND70 PRELIMINARY; PRT; 182 AA.
AC Q8ND70;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein DRFP667B084.
GN Name=DRFP667B084;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
TRISUE=Lymph node;
RC Ansoerge W., Winkner U., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PP2C family.
EMBL: AL834167; CAD38869.1; -.
DR GO: 0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO: 0016787; F:hydrolase activity; IEA.
DR GO: 0000287; F:magnesium ion binding; IEA.
DR GO: 0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO: 0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR000222; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydrolase; Hypothetical protein; Magnesium.
SQ SEQUENCE 182 AA; 20239 MW; 0D2523DE99A810BB CRC64;

Query Match 48.7%; Score 950; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 4.8e-71;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCHTHMEKICMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKICMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180

RESULT 8
Q67UX7 PRELIMINARY; PRT; 348 AA.
ID Q67UX7;
AC Q67UX7;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBa0050G13.3.
GN Name=OSUNBa0050G13.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphorbiaceae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
clone:OSUNBa0050G13.3."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AP005412; BAD38042.1; -.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C SIG; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hypothetical protein.
SQ SEQUENCE 348 AA; 37568 MW; 43405A0F8056495C CRC64;

Query Match 18.9%; Score 369; DB 2; Length 348;
Best Local Similarity 37.5%; Pred. No. 3.1e-22;
Matches 99; Conservative 48; Mismatches 85; Indels 32; Gaps 11;

QY 96 GCASQIGRKENED-----RDFPAQLTDEVLYFAYVDHGGPAAADFCHTHMEKICMDLLP 151
Db 84 GYASAPGKRAMSEDFYETRIDGVD-GETIGLFGVDGHGGAAYEVYKQHL---FSNLIK 139

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QY 152 KEK---NLETLLTLAFLAFLD----KAFSSHARLSADATLLTSGTTATVALLRGIELVVA 204
D 140 HPKFIIDISAIATAETNNHTDSFLKAESHTR-----DAGSTASTAIL-VGDRLVVA 190
QY 205 SVGDSRAILCRKGPVKMLTIDHTPERKDEKERIKKCGGFVAMNSLQOPHVNGLAMTRSI 264
D 191 NVGDSRAVVCRCGDATAVSRRHKPDQDSRQRLEDAGGFVMM--ACTWRVGGVLAVSRAF 248
QY 265 GDLDLTKTSVIAPEPKRIKLHHAADS--FLVTTDGINFMVNSQIEICDFVNOCHDPNEA 322
D 249 GDLKLL-QYVADPE---IKEEIVDSLSLEFLILASDGLWDVNSKEADVVRPIQDPEQA 304
QY 323 AHAVTEQAIQYGTEDNSTAVVVPF 346
D 305 AKRLQEQYQSGADNITVVIVRF 328

RESULT 9
Q8LAY8 PRELIMINARY; PRT; 354 AA.
ID Q8LAY8 AC Q8LAY8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein phosphatase 2C-like protein (hypothetical protein
DE At5g10740/T30N20_10) (Hypothetical protein At5g10740).
GN Names=At5g10740/T30N20_10; Synonyms=At5g10740;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22088475; Pubmed=12093376;
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; genome
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RN SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kaniya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kaniya A., Kawai J., Kim C.-O., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PP2C family.
DR EMBL; AY087522; AA65064.1; -.
DR EMBL; AK117549; BAC42210.1; -.
DR EMBL; BT005431; AAO63851.1; -.
DR HSSP; P35813; 1A60.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.

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DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ Hydrolyase; Hypothetical protein; Magnesium.
KW SEQUENCE 354 AA; 38036 MW; 87DA535B561C9D68 CRC64;

Query Match 18.9%; Score 369; DB 2; Length 354;
Best Local Similarity 36.1%; Pred. No. 3.2e-22; Indels 30; Gaps 11;
Matches 101; Conservative 56; Mismatches 93;

QY 96 GCASQIGKKKENEDRPD--FAQLTDEVL-YFAVYDGHGGPAAADFCHTHWEKCMIMDLPPK 152
D 35 GYASSAGKSSMEDFFETRIDGINGEIVGLFGVFDGCGGARAAYVKRLH---FSNLIITH 91
QY 153 EK---NLETLLTLAFLAFLD----KAFSSHARLSADATLLTSGTTATVALLRGIELVVA 205
D 92 PKFISDTKSAITDAYNHTDSELLKSENHR-----DAGSTASTAIL-VGDRLVVA 142
QY 206 VGDRAILCRKGPVKMLTIDHTPERKDEKERIKKCGGFVAMNSLQOPHVNGLAMTRSIG 265
D 143 VGDRAVTSRGGKATAVSRDHKPDQSDERERENAGGFVMM--AGTWRVGGVLAVSRAF 200
QY 266 DLDLTKTSVIAPEPKRIKLHHAADS--FLVTTDGINFMVNSQIEICDFVNOCHDPNEA 323
D 201 DRLLK-QYVADPEQEEKI---DQLEFLILASDGLWDVFSNEAAVAVKVEDEPDSA 256
QY 324 HAVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSFINEFSR 363
D 257 KKLVGAEIKRGSADNITCVVVRFLKKSSASSSHISSSK 296

RESULT 10
Q9LEW5 PRELIMINARY; PRT; 348 AA.
ID Q9LEW5 AC Q9LEW5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein phosphatase 2C-like protein.
GN Names=T30N20_10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Bevan M., Peters S.A., van Staveren M., Dirkee W., Stiekema W.,
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PP2C family.
DR EMBL; ALJ365234; CAB96829.1; -.
DR PIR; T50783; T50783.
DR HSSP; P35813; 1A60.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolyase; Magnesium.
KW SEQUENCE 348 AA; 37379 MW; 12447BB07F740E2C CRC64;

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Db	135	DSRAVSKGGQGAVERDRHKPDQDTRQRIEDAGGFVMM--AGTWRVGGVLAVSRAPGDK	192			
Qy	268	DKLTSVGVIAEPETPKRIKLHHADDS--FLVLTDTGGINFMVNSQBIICDFVNOCHDPNEAAHA	325			
Db	193	LLKPY-VVADPE---IKEEVDSLSLEFLILASDGLWDVVNEEAVAMVKPIQDPQEAANK	248			
Qy	326	VTEQAIQYGTEDNSTAVVVPF	346			
Db	249	LLEASRRGSSDNITVIIVRF	269			
RESULT 12						
ID	Q9M1P8	PRELIMINARY;	PRT; 383 AA.			
AC	Q9M1P8;					
DT	01-OCT-2000	(TrEMBLrel. 15, Created)				
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)				
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)				
DE	Hypochemical protein T17JL3.220 (Protein phosphatase-2C).					
GN	Name=T17JL3.220;					
OS	Arabidopsis thaliana (Mouse-ear cress).					
OC	Bakayoka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;					
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.					
NCBI_TaxID=3702;						
RN	[1]					
RN	SEQUENCE FROM N.A.					
RP	Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,					
RA	Lemcke K., Mayer K.F.X., Quetier F., Salancubet M.,					
RA	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.					
RL	[2]					
RP	SEQUENCE FROM N.A.					
RA	EU Arabidopsis sequencing project;					
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.					
RL	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=22088475; PubMed=12093376;					
RA	Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,					
RA	Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;					
RT	"Full-length messenger RNA sequences greatly improve genome					
RT	annotation."; RESEARCH0029-RESEARCH0029(2002).					
RL	[4]					
RP	SEQUENCE FROM N.A.					
RA	Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,					
RA	Feldmann K.					
RA	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; ALI38651; CAB71886.1; -.					
DR	EMBL; AY085949; AAM63159.1; -.					
DR	PIR; T48018; T48018.					
DR	HSP; P35813; 1A6Q.					
DR	GO; GO:0003824; Fcatalytic activity; IEA.					
DR	InterPro; IPR000222; PP2C.					
DR	InterPro; IPR001932; PP2C-like.					
DR	Pfam; PF00481; PP2C; 1.					
DR	SMART; SM00332; PP2CC; 1.					
DR	SMART; SM00331; PP2C-SIG; 1.					
DR	PROSITE; PS01032; PP2C; UNKNOWN_1.					
KW	Hypochemical protein.					
SQ	SEQUENCE 383 AA; 41840 MW; 3ED36648FF529C0A CRC64;					
Query Match						
Best Local Similarity 18.3%; Score 357; DB 2; Length 383;						
Matches 110; Conservative 49; Mismatches 107; Indels 74; Gaps 13;						
Qy	40	SSTSEPRCSRFPDGGSGSPATWNFGIWNDRIDEPILLPPSIKYKGPICKISLNVGCAS	99			
Db	50	SLATSPVADIF-PEGDCDPSVLDYI-----PTIRSGS-----FA	82			
Qy	100	QIGKRKENED---RFD-----FAQLTDEVLYFAYVYDGHGGGAADFCHTHMEKCTMD	148			
Db	83	DIGPKRNMDEHTRIIDLSSQVSGSLFELPKPSAFYAVFDGGHGGGAAYVR---ENAIRF	139			

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QY 149 LIPKE-----KNLETLTLTFLAFLIDKAFSSHARLSADATLITSGTTATVALL 195
Db 140 FFEDEQFQPTSEVSVYVEVETSLANFLQADLALAECSISD-----SCGTALTALI 194
QY 196 RGIELVVASVGSRAILCRKPKMLTIDHTPERKDEKERIKKCGFVAVNSLQOPHYN 255
Db 195 -CGRLLMVANAGDCRAVLCKRGRAIDMSBHPINLLERRRVEESGGFIT----NDGYLN 249
QY 256 GRLMTRSTGDLDK-----TSGVIAEPETKRIKLHADDLFLVLTDDGINFVNSQETC 310
Db 250 EVLAVTRALGDWDLKLPKHSQSPLESEPEIKQITLTE-DDEFLVTCDDGIWDLVTSQEAV 308
QY 311 DFV-----NQCHPNEAAHVAETQAIQYGTEDNSTAVVVPF 346
Db 309 SIVRGLNRHNDPTRCARELVNEALGRNSFDNLTAVVVCF 348

RESULT 13
Q653S3 PRELIMINARY; PRT; 352 AA.
AC Q653S3;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein OJ1065_E04.2-1.
GN Names=OJ1065_E04.2-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
RT clone:OJ1065_E04.2";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005090; BAD45938.1; -.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 38579 MW; 43BFFA25B7750FC2 CRC64;

Query Match 18.2%; Score 354.5; DB 2; Length 352;
Best Local Similarity 31.7%; Pred. No. 5.1e-21;
Matches 106; Conservative 45; Mismatches 108; Indels 75; Gaps 11;

QY 96 GCASQIGKREKEDRFDAQLTDE-VLYPAVDGHHGPPAAADFCHTHMEKIMDLLPKEK 154
Db 25 GLASMQGWRITMEDAHTALPRLDECTSFVGVDGHHGKAVSKFCAKHLH---LQVLKNEA 81
QY 155 ----NLETLTLTFLAFLIDKAFSSHARLSADATL----- 183
Db 82 YSSGDLATSVLKSFRRMDEMMKQGRWELAEIGDKQKFTGMLGIIWSPKPGESDKPE 141
QY 184 -----LTSGTTATVALLRDGIELVVASVGSRAILCRKPKMLTIDHTPE 229
Db 142 DTWTEGPHSHFPPTSGTACVARIIND-ELIVANAGDSRCVLSKRAYDLSKDKPD 200
QY 230 RKDEKERIKKCGFVAVNSLQOPHYNGLAMTRISIGDLDLKTSG-----VIAEPETK 281
Db 201 LDAKERILNAGGFIV-----AGRVNGLMLARAIQGMELKQNEFLPAERQIVTAPELN 255
QY 282 RIKLHADDLFLVLTDDGINFVNSQEIQDFVNCQHPDNEAAHVAETQAIQY-----GT 335
Db 256 TVKLSE-DDEFVLACDGIWDCMSQEVVDVFKEMNTEDLSAVCEKLLDHCLAPVSGG 314
QY 336 E--DNSTAVVPPGANGKYKNSEINFSSRSFAS 367
Db 315 DGCDDNMTVIIVK-----KKPSKSAATSTNQSVSS 345

RESULT 14
Q653S4 PRELIMINARY; PRT; 362 AA.
AC Q653S4;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein OJ1065_E04.2-2.
GN Names=OJ1065_E04.2-2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
RT clone:OJ1065_E04.2";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005090; BAD45937.1; -.
KW Hypothetical protein.
SQ SEQUENCE 362 AA; 39620 MW; CE3C007EE376B92C CRC64;

Query Match 18.2%; Score 354.5; DB 2; Length 362;
Best Local Similarity 31.7%; Pred. No. 5.3e-21;
Matches 106; Conservative 45; Mismatches 108; Indels 75; Gaps 11;

QY 96 GCASQIGKREKEDRFDAQLTDE-VLYPAVDGHHGPPAAADFCHTHMEKIMDLLPKEK 154
Db 25 GLASMQGWRITMEDAHTALPRLDECTSFVGVDGHHGKAVSKFCAKHLH---LQVLKNEA 81
QY 155 ----NLETLTLTFLAFLIDKAFSSHARLSADATL----- 183
Db 82 YSSGDLATSVLKSFRRMDEMMKQGRWELAEIGDKQKFTGMLGIIWSPKPGESDKPE 141
QY 184 -----LTSGTTATVALLRDGIELVVASVGSRAILCRKPKMLTIDHTPE 229
Db 142 DTWTEGPHSHFPPTSGTACVARIIND-ELIVANAGDSRCVLSKRAYDLSKDKPD 200
QY 230 RKDEKERIKKCGFVAVNSLQOPHYNGLAMTRISIGDLDLKTSG-----VIAEPETK 281
Db 201 LDAKERILNAGGFIV-----AGRVNGLMLARAIQGMELKQNEFLPAERQIVTAPELN 255
QY 282 RIKLHADDLFLVLTDDGINFVNSQEIQDFVNCQHPDNEAAHVAETQAIQY-----GT 335
Db 256 TVKLSE-DDEFVLACDGIWDCMSQEVVDVFKEMNTEDLSAVCEKLLDHCLAPVSGG 314
QY 336 E--DNSTAVVPPGANGKYKNSEINFSSRSFAS 367
Db 315 DGCDDNMTVIIVK-----KKPSKSAATSTNQSVSS 345

RESULT 15
P2C2 ARATH STANDARD; PRT; 423 AA.
ID P2C2 ARATH
AC O04719;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein phosphatase 2C ABI2 (EC 3.1.3.16) (PP2C) (Absciseic acid-
DE insensitive 2).
GN Name=ABI2; OrderedLocusNames=At5g57050; ORFNames=MHM17.19;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia, and cv. Landsberg erecta;
RC MEDLINE=97308526; PubMed=9165752;
RX Leung J., Merlot S., Giraudat J.;
RT "The Arabidopsis ABSCISIC ACID-INSENSITIVE2 (ABI2) and ABI1 genes
RT encode homologous protein phosphatases 2C involved in abscisic acid
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Db 400 SKDNISVVVVVDLKGIRKPKSKSLN 423

Search completed: June 17, 2005, 00:57:06

Job time : 175 secs

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RT signal transduction."
RL Plant Cell 9:759-771(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RA Rodriguez P.L., Grill E.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63(2000).
CC -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SIMILARITY: Belongs to the PP2C family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; Y08966; CAA70163.1; -
DR EMBL; Y08965; CAA70162.1; -
DR EMBL; Y11840; CAA72538.1; -
DR EMBL; AB024035; BAA97035.1; -
DR HSSP; P35813; 1A6Q.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2CC; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Calcium-binding; Hydrolase; Magnesium; Manganese; Multigene family;
KW Protein phosphatase.
FT CA_BIND 70 81 EF-hand (Potential).
SQ SEQUENCE 423 AA; 48306 MW; 67CAAC76DAS31A71 CRC64;

Query Match 18.2%; Score 354.5; DB 1; Length 423;
Best Local Similarity 30.6%; Pred. No. 6.5e-21;
Matches 99; Conservative 51; Mismatches 99; Indels 75; Gaps 12;

QY 96 GCASQIGKRNEDRPD-----FAQLTDEVL-----YFAYDGHGGPAA 135
Db 114 GVTSICGRPEMEDSVSTIPFLQVSSSLDGRVTNGFNPILSAHFVGVDGHGGSQA 173
QY 136 DFCHTHMEKIMDLLPKEK-----NLETLLTFLAFLIDKAPSSSHARLSADATLL 184
Db 174 NYCRRMHLALTEIVEKEPEFCGDGTWQEKWKALFNSFMRVDSEIETVAHAPE----- 228
QY 185 TSGTTATVALLRDIELVWASVGSRAILCKGKPKMLTIDHTPERKDEKERIKCGG-F 243
Db 229 TVGSTSVVAVFP-THIFVANGDSRAVLCRGKTPALSVDHKPDRDDEAARIEAAGKV 287
QY 244 VANNSLGQPHVNGRLAMTRSIGDLTKTSGVIAPE---TKRIKLHHADDSFLVLTDDGI 300
Db 288 IRWNG---ARVFGVLAMSRISGDRYLKPS-VIPDPEVTSVRRVK-----EDDCLILASDGL 339
QY 301 NFWVNSQEIICDFVNO-----CHDPN-----EAAHVTQEQAIQYG 334
Db 340 WDVMTNEVCDLARKRILLWHKKVAMAGEALLPAEKRGKGDPAAMSAAYLSKVALQKG 399
QY 335 TEDNSTAVVVPFGAWGKYKNSIN 358
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# OM protein - protein search, using sw model

Run on: June 17, 2005, 00:57:16 ; Search time 160 Seconds  
(without alignments)  
892.752 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSGNQVRRR.....KNSINFSPSPASSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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13	1951	100.0	372	15	US-10-311-764-1	Sequence 1, Appli
14	1951	100.0	372	16	US-10-716-488-2	Sequence 2, Appli
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## ALIGNMENTS

RESULT 1  
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; Patent No. US20020106676A1  
; GENERAL INFORMATION:  
; APPLICANT: Roch, Jean-Marc  
; APPLICANT: Bartel, Paul L.  
; APPLICANT: Helchman, Karen  
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative  
; FILE REFERENCE: Protein Interactions in ND  
; CURRENT APPLICATION NUMBER: US/09/973,963  
; CURRENT FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US 60/240,790  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: US 60/304,775  
; PRIOR FILING DATE: 2001-07-13  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 372  
; TYPE: PRT  
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US-09-973-963-4

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RESULT 2
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; Patent No. US2002010673A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,064
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
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US-09-973-064-4

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; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,077
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-077-4

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; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
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; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,063
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
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US-09-973-063-4

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; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; NUMBER OF SEQ ID NOS: 8
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; ORGANISM: Homo sapiens
US-09-973-964-4

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Best Local Similarity 100.0%; Pred. No. 1e-194;
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; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
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US-09-973-964-4

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; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/975,072
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
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; SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-975-072-4

Query Match      100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 FRSFASGRWA 372

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Qy	301	NFMVNSQEICDFVQNCHDPNEAAHAHVTSQAQYGTEDNSTAVVVPFGAWGKYKNSINFS	360
Db	301	NFMVNSQEICDFVQNCHDPNEAAHAHVTSQAQYGTEDNSTAVVVPFGAWGKYKNSINFS	360
Qy	361	FSRSFASGRWA	372
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RESULT 7  
US-09-972-038-4  
; Sequence 4, Application US/09972038  
; Patent No. US20020119155A1  
; GENERAL INFORMATION:  
; APPLICANT: Roch, Jean-Marc  
; APPLICANT: Bartel, Paul L.  
; APPLICANT: Heichman, Karen  
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative  
; TITLE OF INVENTION: Diseases  
; FILE REFERENCE: Protein Interactions in ND  
; CURRENT APPLICATION NUMBER: US/09/972,038  
; CURRENT FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 60/240,790  
; PRIOR FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-038-4

RESULT 8  
US-09-972-757-4  
; Sequence 4, Application US/09972757

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; Patent No. US20020119927A1
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; GENERAL INFORMATION:
;
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
;
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
;
; TITLE OF INVENTION: Diseases
;
; FILE REFERENCE: Protein Interactions in ND
;
; CURRENT APPLICATION NUMBER: US/09/972,757
;
; CURRENT FILING DATE: 2001-10-09
;
; PRIORITY APPLICATION NUMBER: US 60/240,790
;
; PRIOR FILING DATE: 2000-10-17
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; NUMBER OF SEQ ID NOS: 4
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; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 4
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; LENGTH: 372
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; TYPE: PRT
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; ORGANISM: Homo sapiens
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; US-09-972-757-4

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RESULT 9
US-09-973-965-4
; Sequence 4, Application US/09973965
; Patent No. US20020124273A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,965
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

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; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-965-4

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Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNTLTLTAFLEIDKAFSSHARLSAD 180

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QY 241 GGFVANNLSGQPHVNGRLAMTRISIGDLKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300
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QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 10
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US20020164655A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-941-4

Query Match      100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 11
US-09-986-992-2
; Sequence 2, Application US/09986992
; Publication No. US20030027308A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; FILE REFERENCE: GENOMIC SEQUENCING
; CURRENT APPLICATION NUMBER: US/09/986,992
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/246,974
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/208,291
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-992-2

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Best Local Similarity 100.0%; Pred. No. 1e-194;
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Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKKC 240

QY 241 GGFVANNLSGQPHVNGRLAMTRISIGDLKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300
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QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
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RESULT 12  
 US-09-971-782-4  
 ; Sequence 4, Application US/09971782  
 ; Publication No. US20030186317A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roch, Jean-Marc  
 ; APPLICANT: Bartel, Paul L.  
 ; APPLICANT: Heichman, Karen  
 ; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative  
 ; FILE REFERENCE: Protein Interactions in ND  
 ; CURRENT APPLICATION NUMBER: US/09/971,782  
 ; CURRENT FILING DATE: 2001-10-09  
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 ; ORGANISM: Homo sapiens  
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 ; US-09-971-782-4

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RESULT 13  
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 ; Sequence 1, Application US/10311764  
 ; Publication No. US20040023245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
 ; APPLICANT: BAUGHN, Mariah R.; DING, Li  
 ; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.  
 ; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.

; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.  
 ; APPLICANT: LU, Yan; NGUYEN, Daniel B.  
 ; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
 ; APPLICANT: REDDY, Roopa M.; SANOJANWALA, Madhusudan M.  
 ; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
 ; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.  
 ; APPLICANT: CHAWLA, Narinder K.; YANG, Junming  
 ; APPLICANT: YAO, Monique G.; YUE, Henry  
 ; TITLE OF INVENTION: PROTEIN PHOSPHATASES  
 ; FILE REFERENCE: PI-0126 USN  
 ; CURRENT APPLICATION NUMBER: US/10/311,764  
 ; CURRENT FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US01/19442  
 ; PRIOR FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/212,447  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/213,746  
 ; PRIOR FILING DATE: 2000-06-22  
 ; PRIOR APPLICATION NUMBER: US 60/215,210  
 ; PRIOR FILING DATE: 2000-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/216,529  
 ; PRIOR FILING DATE: 2000-07-06  
 ; PRIOR APPLICATION NUMBER: US 60/218,080  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/220,117  
 ; PRIOR FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1  
 ; LENGTH: 372  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
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 ; US-10-311-764-1

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 Db 61 WDNFGIWNDRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120  
 QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNETLLTLAFLIDKAFSSHARLSAD 180  
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 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 Db 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
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 Db 241 GGFVAVNSLQGPVHNGRLAMTRISIGDLDLKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 300  
 QY 301 NFVNSQEI CDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINF 360  
 Db 301 NFVNSQEI CDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINF 360  
 QY 361 FSRSPASSGRWA 372  
 Db 361 FSRSPASSGRWA 372

RESULT 14  
 US-10-716-488-2  
 ; Sequence 2, Application US/10716488





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 00:50:20 ; Search time 42 Seconds  
(without alignments)  
661.177 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSGNQVRRR.....KNSINFSPASSGRWA 372

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	325	16.7	281	3	US-08-935-855-9
4	325	16.7	281	4	US-08-938-092-91
5	319.5	16.4	390	2	US-08-873-093-3
6	319.5	16.4	390	4	US-09-206-646-3
7	314	16.1	392	4	US-09-013-881-2
8	314	16.1	392	4	US-09-612-473-2
9	314	16.1	392	4	US-09-724-730-2
10	307.5	15.8	382	4	US-09-538-092-1086
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13	307.5	15.8	458	4	US-09-949-016-7534
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17	300	15.4	309	3	US-08-935-855-7
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19	290.5	14.9	454	4	US-09-538-092-1156
20	282.5	14.5	478	2	US-08-873-093-1
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27	279	14.3	314	2	US-08-822-701-10

ALIGNMENTS

RESULT 1

US-09-973-963-4

; Sequence 4, Application US/09973963

; Patent No. 6653102

; GENERAL INFORMATION:

; APPLICANT: Roch, Jean-Marc

; APPLICANT: Bartel, Paul L.

; APPLICANT: Heichman, Karen

; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative

; TITLE OF INVENTION: Diseases

; FILE REFERENCE: Protein Interactions in ND

; CURRENT APPLICATION NUMBER: US/09/973,963

; CURRENT FILING DATE: 2001-10-11

; PRIOR APPLICATION NUMBER: US 60/240,790

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: US 60/304,775

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 372

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-973-963-4

Query Match 100.0%; Score 1951; DB 4; Length 372;

Best Local Similarity 100.0%; Pred. No. 7e-193;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	WDNFGIWDNRIDPILLPPSIKYGKPIKISLENVGCSAIOIGKRNEDRDFQAQLTDEV	120
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Db	121	LYFAVYDGHGHPAAADFCHTHMEKIMDILPKENLETLLTFLAFLEIDKAFSSHARLSAD	180
Qy	181	ATLLTSGTTATVALLRDGIELVWASGDSRAILCKGKPKMLTIDHTPERKDEKERIKC	240
Db	181	ATLLTSGTTATVALLRDGIELVWASGDSRAILCKGKPKMLTIDHTPERKDEKERIKC	240
Qy	241	GGFVANNLGGPHVNGRLAMTRISGIDLKTSVGVIARPETKRIKLHADDLSFLVLTDDGI	300
Db	241	GGFVANNLGGPHVNGRLAMTRISGIDLKTSVGVIARPETKRIKLHADDLSFLVLTDDGI	300
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Query Match	16.7%; Score 325; DB 3; Length 281;
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	CITY: Palo Alto	
	STATE: CA	
	COUNTRY: USA	
	ZIP: 94304	
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	MEDIUM TYPE: Diskette	
	COMPUTER: IBM Compatible	
	OPERATING SYSTEM: DOS	
	SOFTWARE: FASTSEQ for Windows Version 2.0	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/08/873,093	
	FILING DATE: Filed Herewith	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	
	FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Billings, Lucy J.	
	REGISTRATION NUMBER: 36,749	
	REFERENCE/DOCKET NUMBER: PF-0319 US	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 415-855-0555	
	TELEFAX: 415-845-4166	
	INFORMATION FOR SEQ ID NO: 3:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 390 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	IMMEDIATE SOURCE:	
	LIBRARY: GenBank	
	CLONE: 1247927	
	US-08-873-093-3	

	CITY: Palo Alto	
	STATE: CA	
	COUNTRY: USA	
	ZIP: 94304	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Diskette	
	COMPUTER: IBM Compatible	
	OPERATING SYSTEM: DOS	
	SOFTWARE: FASTSEQ for Windows Version 2.0	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/08/873,093	
	FILING DATE: Filed Herewith	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	
	FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Billings, Lucy J.	
	REGISTRATION NUMBER: 36,749	
	REFERENCE/DOCKET NUMBER: PF-0319 US	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 415-855-0555	
	TELEFAX: 415-845-4166	
	INFORMATION FOR SEQ ID NO: 3:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 390 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	IMMEDIATE SOURCE:	
	LIBRARY: GenBank	
	CLONE: 1247927	
	US-08-873-093-3	

	CITY: Palo Alto	
	STATE: CA	
	COUNTRY: USA	
	ZIP: 94304	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Diskette	
	COMPUTER: IBM Compatible	
	OPERATING SYSTEM: DOS	
	SOFTWARE: FASTSEQ for Windows Version 2.0	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/08/873,093	
	FILING DATE: Filed Herewith	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	
	FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Billings, Lucy J.	
	REGISTRATION NUMBER: 36,749	
	REFERENCE/DOCKET NUMBER: PF-0319 US	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 415-855-0555	
	TELEFAX: 415-845-4166	
	INFORMATION FOR SEQ ID NO: 3:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 390 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	IMMEDIATE SOURCE:	
	LIBRARY: GenBank	
	CLONE: 1247927	
	US-08-873-093-3	

	CITY: Palo Alto	
	STATE: CA	
	COUNTRY: USA	
	ZIP: 94304	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Diskette	
	COMPUTER: IBM Compatible	
	OPERATING SYSTEM: DOS	
	SOFTWARE: FASTSEQ for Windows Version 2.0	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/08/873,093	
	FILING DATE: Filed Herewith	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	
	FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Billings, Lucy J.	
	REGISTRATION NUMBER: 36,749	
	REFERENCE/DOCKET NUMBER: PF-0319 US	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 415-855-0555	
	TELEFAX: 415-845-4166	
	INFORMATION FOR SEQ ID NO: 3:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 390 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	IMMEDIATE SOURCE:	
	LIBRARY: GenBank	
	CLONE: 1247927	
	US-08-873-093-3	

	CITY: Palo Alto	
	STATE: CA	
	COUNTRY: USA	
	ZIP: 94304	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Diskette	
	COMPUTER: IBM Compatible	
	OPERATING SYSTEM: DOS	
	SOFTWARE: FASTSEQ for Windows Version 2.0	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/08/873,093	
	FILING DATE: Filed Herewith	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	
	FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Billings, Lucy J.	
	REGISTRATION NUMBER: 36,749	
	REFERENCE/DOCKET NUMBER: PF-0319 US	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 415-855-0555	
	TELEFAX: 415-845-4166	
	INFORMATION FOR SEQ ID NO: 3:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 390 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	IMMEDIATE SOURCE:	
	LIBRARY: GenBank	
	CLONE: 1247927	
	US-08-873-093-3	

	CITY: Palo Alto	
	STATE: CA	
	COUNTRY: USA	
	ZIP: 94304	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Diskette	
	COMPUTER: IBM Compatible	
	OPERATING SYSTEM: DOS	
	SOFTWARE:	

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; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: ID No. 6436637 g247927
US-09-206-646-3

Query Match      16.4%; Score 319.5; DB 4; Length 390;
Best Local Similarity 31.6%; Pred. No. 3.2e-24;
Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;

QY 88 PKISLENV-----GCASQIGKKEKEDR-----FDFQLTDEVLVYFAYVDGCHGPPAA 134
Db 8 PKTEKNAHGAGNGLRYGLSSMGWRVEMEDAHTAVVGIPHGLEDWSFFAYVDGCHGSRV 67
QY 135 ADFCHTHM-----EKIMDLPKKNLETLTLTFLAFLDKAFSSSHARLSADA 181
Db 68 ANYCSTHLEHITNEDFRAADKSGFALEPSVENKIGTGLKIDENYRNFSDLNG- 126
QY 182 TLTSGTTATVALLRDIELVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKCG 241
Db 127 -MDRSGSTA-VGWMISPTHIYFINGDSRAVLCRNGQVCFSTQDHPKPCNPMERIKQAG 184
QY 242 GFVAMNSLGOPHVNGLAMTRSGDLDLK-----TSGVIA-EPETKRIKLHADDSPFL 293
Db 185 G-----SVMTQRVNGSLAVSRALGDYDKVDGKGPTQLVSPPEYVEI-LRAEEDFV 238
QY 294 VLTTDGINFMVNSQICDFVQ-----CHDPNEAAHVAHQAIQVGTEDNSTAVVVPF 346
Db 239 VLACDGIWVNSNEELCEFFVNSRLEVSDDLENVCNVMVDTCLHKGGRDNMSIVLVCF 295

RESULT 7
US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 195647
US-09-013-881-2

Query Match      16.1%; Score 314; DB 3; Length 392;
Best Local Similarity 27.5%; Pred. No. 1.2e-23;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LQDDRRVPTCHSSTSEPRCSRFDPDGSGSPATWNFGIWDRIDEPIILLPSI----- 81
Db 27 LIFDD---LPPASSTDS-----GSGGPLLFD-----LPPASSGDSG 60
QY 82 -----KYG-----KPIPKISLENVGCASQIGKRK-ENED 109
Db 61 SLATSISQWVKTEGKAKRKTSEEEKNGSEELVEKVKCRASSVIFGLKGYVAERKGEREE 120
QY 110 RPD-----FQALTD-----VLVYFAYVDGCHGPPAAADFCHTHMEKCIMDLPK--- 152
Db 121 MQDAHVILNDITEECRPPSSLIRVSYFAVFDGHHGIRASKFAAQNHLHQLIRKFPKGDV 180
QY 153 -----EKPLETLTLTFLAFLDKAFSSSHARLSADATLTLTSGTTATVALLRDIELVVASVGD 209
Db 181 ISVEKTVKCLLDTFKHTEDEFLKQA--SSQKPAWKGSGTATCVLAVDNI-LYIANLGDS 237
QY 210 RAILCR-----KGKPMKLTIDHTPERKDEKERIKKCGGFVAMNSLGOPHVNGLAMTR 263
Db 238 RAILCRYNESOKHAALSLSKEHNPTQYERMRIQKAGG-----NVRDGRVLGVLEVSRS 292
QY 264 IGDLDLKTSGVTAEPETKRIKLHADDSPFLVLTDDGINFMVNSQICDFVNOCHDPNE-- 321
Db 293 IGDQYKRCGVTSVPDIRRQCL--TPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351
QY 322 -----AAHVAHQAIQVGTEDNSTAVVVPFG 347
Db 352 TREKSAADARYEAACNRLANKAVQSGADNVTVMVVRIG 391

RESULT 8
US-09-612-473-2
; Sequence 2, Application US/09612473
; Patent No. 6518029
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/09/612,473
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6518029 195647
US-09-612-473-2

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239  VILADGWDVRSNEETCEF VASRKUEVSUDDLEVLNWNVVDICHHKSSKDNMSVVLVLCF 239

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RESULT 13  
 US-09-949-016-7534  
 ; Sequence 7534, Application US/09949016  
 ; Patent NO. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7534  
 ; LENGTH: 458

[illegible]

DD 314 CDGLWDVMGNEELCDFVKSKLEVIDDDLEKVCNEVVDCLTAGSKDNMSVILICF 367

RESULT 14  
US-08-822-701-8



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; Sequence 8, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
; US-08-822-701-8

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Query Match 15.7%; Score 306.5; DB 2; Length 306;
Best Local Similarity 31.0%; Pred. No. 4.8e-23;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

Qy 88 PKISLENV-----GCASQIGKRNEDR----FDFAQLTDEVLYFAYVDGHPAA 134
Db 8 PKMEKHNAQGGNGRLRYGLSSMOGWRVEMEDAHAVIGLPSGLTWSFFAVYDGHAGSQV 67

Qy 135 ADFCHTMEKIMDL-----LPKEKNLETLTLAFLAIDK--AFSSSHARLSADATLL 184
Db 68 AKYCEHLLDHIITNNQDFKGSAGAPSVENKNGIRGTGFLAIDHMRVMSEKKGAD---- 123

Qy 185 TSGTTATVALLRDIQELVWASVGSRAILCRKGPMLTIDHTPERKDEKERIKKCGFV 244
Db 124 RSGSTA-VGVLLISPOHTYFINGDSRGLLCNRKRVHFFTDQHKPSNPLEKERIQWAG-- 180

Qy 245 AWWSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHHADSFVLIT 296
Db 181 ---SVMTQRVNGSLAVSRALGDFDKVHGKGPTEQLVSPPEVHDIERSEDDQFIILA 237

Qy 297 TDGINFMVNSOEICDFVNO-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
Db 238 CDGIWDVWGNEELCDFVRSRLVETDDEKVCNEVVDTCLYKGRSDNMSVILICF 291

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RESULT 15
US-08-935-855-8
; Sequence 8, Application US/08935855

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; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
; US-08-935-855-8

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Query Match 15.7%; Score 306.5; DB 3; Length 306;
Best Local Similarity 31.0%; Pred. No. 4.8e-23;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

Qy 88 PKISLENV-----GCASQIGKRNEDR----FDFAQLTDEVLYFAYVDGHPAA 134
Db 8 PKMEKHNAQGGNGRLRYGLSSMOGWRVEMEDAHAVIGLPSGLTWSFFAVYDGHAGSQV 67

Qy 135 ADFCHTMEKIMDL-----LPKEKNLETLTLAFLAIDK--AFSSSHARLSADATLL 184
Db 68 AKYCEHLLDHIITNNQDFKGSAGAPSVENKNGIRGTGFLAIDHMRVMSEKKGAD---- 123

Qy 185 TSGTTATVALLRDIQELVWASVGSRAILCRKGPMLTIDHTPERKDEKERIKKCGFV 244
Db 124 RSGSTA-VGVLLISPOHTYFINGDSRGLLCNRKRVHFFTDQHKPSNPLEKERIQWAG-- 180

Qy 245 AWWSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHHADSFVLIT 296
Db 181 ---SVMTQRVNGSLAVSRALGDFDKVHGKGPTEQLVSPPEVHDIERSEDDQFIILA 237

Qy 297 TDGINFMVNSOEICDFVNO-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
Db 238 CDGIWDVWGNEELCDFVRSRLVETDDEKVCNEVVDTCLYKGRSDNMSVILICF 291

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Search completed: June 17, 2005, 00:58:39
Job time : 44 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 00:38:39 ; Search time 163 Seconds  
(without alignments)

882.668 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTFAALITLVRSGGNQVRRR.....KNSINFSPSPASSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1980s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1951	100.0	372	5	AAE23954 PN7740 pr
2	1951	100.0	372	5	Abb79999 Human pho
3	1951	100.0	372	5	Abg70789 Fe65 inte
4	1951	100.0	372	5	AAE23953 PN7740 pr
5	1951	100.0	372	5	Abg70801 Fe65 inte
6	1951	100.0	372	5	Abg70826 Fe65 inte
7	1951	100.0	372	5	Abb07402 Human pro
8	1951	100.0	372	5	AAE23976 Human PN7
9	1951	100.0	372	5	AAE24078 Human PN7
10	1951	100.0	372	5	AAE14451 Human pro
11	1951	100.0	372	6	ABU10309 Human pro
12	1951	100.0	372	6	AAO23055 Human ser
13	1951	100.0	372	7	ADB66824 Human PN7
14	1951	100.0	372	7	ADJ73452 Novel hum
15	1951	100.0	372	8	ADQ14718 Human pro
16	1951	100.0	372	8	ADR30806 Human ser
17	1950	99.9	372	6	ADA54131 Human pro
18	1950	99.9	372	7	ADJ70681 Human hea
19	1950	99.9	372	8	ADN05534 Antipsori
20	1939	99.4	373	4	AAU22934 Novel hum
21	1924	98.6	373	3	AAE57077 Human pro
22	1921	98.5	404	8	ABM83874 Human dia
23	1809	92.7	351	5	ABB07401 Human pro
24	1777	91.1	372	7	ADF53640 Murine ph
25	1727	88.5	352	5	Abb78059 Amino aci

#### ALIGNMENTS

##### RESULT 1

AAE23954  
ID AAE23954 standard; protein; 372 AA.

XX AAE23954;

XX 23-SEP-2002 (first entry)

XX PN7740 protein.

XX Protein-protein interaction; neurodegenerative disorder; dementia;

XX Huntington's disease; Parkinson's disease; Alzheimer's disease; AD;

XX protein therapy; drug screening.

XX Unidentified.

XX WO200233114-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032199.

XX 17-OCT-2000; 2000US-0240790P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Roch J, Bartel PL, Heichman K;

XX WPI; 2002-454603/48.

XX N-PSDB; AAD38600.

XX New protein complexes involved in neurodegenerative diseases, useful for  
diagnosing the presence of or a predisposition to a neurodegenerative  
disorders (e.g. Alzheimer's) or in screening for drugs for treating the  
diseases.

XX Example 6; Page 52; 93pp; English.

XX The invention relates to the discovery of protein-protein interactions  
that are involved in the pathogenesis of neurodegenerative disorders,  
including Alzheimer's disease (AD). The invention is also directed to  
protein complexes involved in neurodegenerative disorders. The protein  
complexes are useful for diagnosing the presence of or a predisposition  
to neurodegenerative disorders (e.g. Huntington's disease, Parkinson's  
disease, dementia and Alzheimer's disease). They are also useful in drug  
screening. The invention is used in protein therapy. The present sequence  
is PN7740 protein. This sequence is used in the exemplification of the  
invention

Ade31687 Human 161  
Abb07392 Human pro  
Abq06716 Novel hum  
Abg28412 Novel hum  
Aam41604 Human pol  
Aab47431 Human pro  
Aam39818 Human pol  
Ada55670 Human pro  
Abb07393 Human pro  
Abb07397 Human pro  
Adi17317 Polypepti  
Adi17318 Polypepti  
Aag06997 Arabidops  
Aag09824 Arabidops  
Adn73999 Thale cre  
Aae01345 Arabidops  
Abb07400 Amino aci  
Aae04841 Human SGP  
Aau75784 Human pro  
Abb78060 Consensus

26 1727 88.5 352 7 ADE31687  
27 1538.5 78.9 373 5 ABB07392  
28 1375.5 70.5 1072 4 ABG06716  
29 1375.5 70.5 1195 4 ABG28412  
30 1150 58.9 238 4 AAM41604  
31 951.5 48.8 233 4 AAB47431  
32 814 41.7 153 4 AAM39818  
33 790 40.5 150 6 ADA55670  
34 669.5 34.3 156 5 ABB07393  
35 437 22.4 83 5 ABB07397  
36 412.5 21.1 260 5 ADI17317  
37 395.5 20.3 252 5 ADI17318  
38 369 18.9 354 3 AAG06997  
39 357 18.3 383 3 AAG09824  
40 357 18.3 383 8 ADN73999  
41 354.5 18.2 423 4 AAE01345  
42 354.5 18.2 423 5 ABB07400  
43 350.5 18.0 360 4 AAE04841  
44 350.5 18.0 360 5 AAU75784  
45 350 17.9 274 5 ABB78060

XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60  
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120  
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120

QY 121 LYPAVYDGHGGPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180  
DB 121 LYPAVYDGHGGPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRSIGDLTKTSGLVIAEPETKRIKLHHADDSFLVLTDDGI 300  
DB 241 GGFVAVNSLGQPHVNGRLAMTRSIGDLTKTSGLVIAEPETKRIKLHHADDSFLVLTDDGI 300

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

QY 361 FSRSFASSGRWA 372  
DB 361 FSRSFASSGRWA 372

RESULT 2  
ABB79999  
ID ABB79999 standard; protein; 372 AA.

XX AC ABB79999;  
XX DT 19-DEC-2002 (first entry)  
XX DE Human phosphatase PN7740.  
XX KW PN7740; phosphatase; enzyme; human neurodegenerative disease;  
XX KW Alzheimer's disease; dementia; Parkinson's disease; Huntington's disease;  
XX KW diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT Domain 104..339  
XX FT /note= "phosphatase 2C domain"

XX PN US2002115607-A1.  
XX PD 22-AUG-2002.  
XX PF 12-OCT-2001; 2001US-00975072.  
XX PR 17-OCT-2000; 2000US-0240790P.  
XX PA (MYRI-) MYRIAD GENETICS INC.  
XX PI Roch J, Bartel PL, Heichman K;  
XX DR WPI; 2002-722778/78.  
XX DR N-PSDB; ABQ81507.  
XX PT New protein complex useful for treating neurodegenerative disease e.g.  
XX PT Alzheimer's, comprises two proteins or their fragments, for e.g. BA13

PT with glypican, LRP2, LRPAP1 or transthyretin.  
XX Example 2-33; Page 23; 41pp; English.

XX The present sequence is the protein sequence of a novel human  
CC phosphatase, designated PN7740. The sequence is predicted from a human  
CC brain cDNA clone identified in a yeast two-hybrid screening using as bait  
CC a fragment of Fe65 protein (amino acids 360-552, i.e. the first  
CC phosphotyrosine binding domain (PTB)). Identification of a phosphatase 2C  
CC PTB of Fe65. Pharmacological modulation of this interaction may influence  
CC amyloid beta protein precursor metabolism. The invention provides protein  
CC complexes, identified by yeast two-hybrid screening, that comprise 2  
CC interacting proteins (or fragments), antibodies to the complexes,  
CC diagnosis of neurodegenerative disorders (including diagnosis of a  
CC predisposition to, or existence of, the disorder), drug screening for  
CC agents which modulate the protein interaction, and identification of  
CC additional proteins in the pathway common to the interacting proteins. A  
CC claimed method for treating a neurodegenerative disorder selected from  
CC Huntington's disease, Parkinson's disease, dementia and Alzheimer's  
CC disease involves administering a compound capable of modulating the  
CC protein complex. The compound may interfere with the protein interaction,  
CC bind one of the 2 proteins, may be an antibody immunoreactive with one of  
CC the proteins, or a nucleic acid encoding such an antibody, or is a  
CC compound that modulates expression of one of the proteins, is an  
CC antisense compound or ribozyme which hybridises to a nucleic acid  
CC encoding one of the proteins, or is a compound capable of strengthening  
CC the protein interaction (all claimed)

XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60  
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120  
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120

QY 121 LYPAVYDGHGGPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180  
DB 121 LYPAVYDGHGGPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRSIGDLTKTSGLVIAEPETKRIKLHHADDSFLVLTDDGI 300  
DB 241 GGFVAVNSLGQPHVNGRLAMTRSIGDLTKTSGLVIAEPETKRIKLHHADDSFLVLTDDGI 300

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

QY 361 FSRSFASSGRWA 372  
DB 361 FSRSFASSGRWA 372

RESULT 3  
ABG70789  
ID ABG70789 standard; protein; 372 AA.  
XX AC ABG70789;  
XX DT 12-DEC-2002 (first entry)  
XX DE Fe65 interacting human protein, PN7740, protein.

XX Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MLK2;  
 KW mixed lineage kinase 2; ligand; transporter; cellular uptake;  
 KW neuronal death; neurodegenerative disorder; Huntington's disease;  
 KW Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS1;  
 KW PS2; Abeta; trophic; sAPP; metabolite; Fe65.  
 XX Homo sapiens.  
 XX US20021119927-A1.  
 XX 29-AUG-2002.  
 XX 09-OCT-2001; 2001US-00972757.  
 XX 17-OCT-2000; 2000US-0240790P.  
 XX (MYRI-) MYRIAD GENETICS INC.  
 XX Roch J, Bartel PL, Heichman K;  
 DR N-PSDB; ABS5204.  
 XX  
 XX Modulating protein complex having proteins which is CIB interacting with  
 PT mixed lineage kinase 2, in a cell, by administering compound that  
 PT modulates the complex, or peptide that interferes interaction between  
 PT proteins.  
 XX Example 6; Page 22; 37pp; English.  
 XX The invention discloses a method for modulating in a cell, a protein  
 CC complex having a first protein, which is CIB (calcium-binding protein),  
 CC interacting with a second protein, which is mixed lineage kinase (MLK)2,  
 CC or the interaction of MLK2 with the ligand, which comprises administering  
 CC to the cell a compound capable of modulating the protein complex or the  
 CC interaction, or a peptide capable of interfering with the protein's  
 CC interactions. The peptide is associated with a transporter capable of  
 CC increasing cellular uptake of the peptide. The method is useful for  
 CC modulating neuronal death in a patient having a neurodegenerative  
 CC disorder such as Huntington's disease, Parkinson's disease, dementia and  
 CC Alzheimer's disease. The technique used to discover additional proteins  
 CC that interact with the major Alzheimer's disease proteins (including APP,  
 CC not defined, and presenilins) was the yeast two-hybrid system. CIB has  
 CC been shown to interact with the presenilins, PS1 and PS2, but due to the  
 CC casual role of mutations of these presenilins in Alzheimer's disease,  
 CC other proteins, like MLK2, are likely to play a major role in the  
 CC pathogenesis. APP metabolism is also a critical event in Alzheimer's  
 CC disease pathogenesis as it leads to the release of either toxic (Abeta)  
 CC or trophic (sAPP) metabolites. Fe65 (not defined) has been shown to  
 CC interact with APP and peptides interacting with Fe65 may also be useful  
 CC in treating neurodegenerative disorders. The compound may be capable of  
 CC strengthening the interaction between the first and the second protein.  
 CC The sequence presented is the human PN7740 protein which was isolated due  
 CC to its interaction with Fe65 found using the yeast two-hybrid system  
 XX  
 XX Sequence 372 AA;  
 Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSTAALTLVRSNGVRRRLVLSRLQDDRRVPTCHSTSTSPRCSPFDDGSGSPAT 60  
 Db 1 MSTAALTLVRSNGVRRRLVLSRLQDDRRVPTCHSTSTSPRCSPFDDGSGSPAT 60  
 Qy 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGASQIGKKNEDRDFDQALITDEV 120  
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGASQIGKKNEDRDFDQALITDEV 120  
 Qy 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLLTFLAFLIDKAFSSHARLSAD 180  
 Db 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLLTFLAFLIDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 Qy 241 GGFVAVNSLQGFVNGRLAMTRISIGDLDLKTSGLVIAPEPTKRIKLHHADDSFLVLTDDGI 300  
 Db 241 GGFVAVNSLQGFVNGRLAMTRISIGDLDLKTSGLVIAPEPTKRIKLHHADDSFLVLTDDGI 300  
 Qy 301 NFWNSQEIICDFVNOCHDPNEAAHVAHQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
 Db 301 NFWNSQEIICDFVNOCHDPNEAAHVAHQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
 Qy 361 FRSFASGGRWA 372  
 Db 361 FRSFASGGRWA 372  
 RESULT 4  
 AAE23953  
 ID AAE23953 standard; protein; 372 AA.  
 XX  
 AC AAE23953;  
 XX  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE PN7740 protein.  
 XX  
 KW Protein-protein interaction; neurodegenerative disorder; CIB; MLK2;  
 KW Alzheimer's disease; calcium binding protein; mixed lineage kinase 2;  
 KW Huntington's disease; dementia; Parkinson's disease; AD.  
 XX Unidentified.  
 OS  
 XX WO200233112-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032196.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Roch J, Bartel PL, Heichman K;  
 XX  
 DR WPI; 2002-454607/48.  
 DR N-PSDB; AAD38594.  
 XX  
 PT New protein complex comprising CIB and mixed lineage kinase 2, useful as  
 PT targets for diagnostic tools in identifying individuals at risk for  
 PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's  
 PT disease or dementia.  
 XX  
 PS Example 6; Page 52; 91pp; English.  
 XX  
 CC The invention relates to the discovery of protein-protein interactions  
 CC that are involved in the pathogenesis of neurodegenerative disorders  
 CC including Alzheimer's disease (AD). The invention is also directed to  
 CC protein complex comprising two proteins selected from a complex of  
 CC calcium binding protein (CIB) and mixed lineage kinase 2 (MLK2). AD  
 CC interacting proteins are useful as new targets for the identification of  
 CC useful pharmaceuticals, new targets for diagnostic tools in the  
 CC identification of individuals at risk, sequences for producing  
 CC transformed cell lines, cellular models and animal models and new bases  
 CC for therapeutic intervention in neurodegenerative disorders, including.  
 CC Modulators of the protein complex are useful for treating  
 CC neurodegenerative disorders including Huntington's disease, dementia,  
 CC Parkinson's disease and AD. The present sequence is PN7740 protein. This  
 CC sequence used in the exemplification of the invention  
 XX  
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206; Mismatches 0; Indels 0; Gaps 0;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60  
 DB 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIPKISLNVGCSQIGKRKKNEDRFDFAQLTDEV 120  
 DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIPKISLNVGCSQIGKRKKNEDRFDFAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHHADDSFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHHADDSFLVLTDDGI 300

QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 DB 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360

QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 5  
 ABG70801  
 ID ABG70801 standard; protein; 372 AA.  
 AC ABG70801;  
 XX  
 DT 16-DEC-2002 (first entry)  
 XX  
 DE Fe65 interacting human protein, PN7740, protein.  
 XX  
 KW Yeast two-hybrid; PN7740; human; Mint2; PDE-9A; KIAA0427; ligand;  
 KW transporter; cellular uptake; neuronal death; neurodegenerative disorder;  
 KW Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease;  
 KW APP; presenilin; Abeta; trophic; sAPP; metabolite; Fe65.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002114799-A1.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PF 10-OCT-2001; 2001US-00973077.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Roch J, Bartel PL, Heichman K;  
 XX  
 DR WPI; 2002-740090/80.  
 DR N-PSDB; ABS55222.  
 XX  
 XX Modulating protein complex having Mint2 interacting with PDE-9A, by  
 PT administering compound capable of modulating protein complex, or peptide  
 PT capable of interfering with protein-protein interaction.  
 XX  
 XX Example 6; Page 22; 37pp; English.  
 PS  
 XX The invention discloses a method for modulating in a cell, a protein  
 CC complex having a first protein, which is Mint2, interacting with a second  
 CC

CC protein, which is PDE-9A, or the interaction of PDE-9A with the ligand,  
 CC which comprises administering to the cell a compound capable of  
 CC modulating the protein complex or the interaction, or a peptide capable  
 CC of interfering with the protein's interactions. The peptide is associated  
 CC with a transporter capable of increasing cellular uptake of the peptide.  
 CC The method is useful for modulating neuronal death in a patient having a  
 CC neurodegenerative disorder such as Huntington's disease, Parkinson's  
 CC disease, dementia and Alzheimer's disease. The technique used to discover  
 CC additional proteins that interact with the major Alzheimer's disease  
 CC proteins (including APP, not defined, and presenilins) was the yeast two-  
 CC hybrid system. Mint2 has been shown to interact with APP, and due to its  
 CC interaction with presenilins and KIAA0427 it is likely to play a major  
 CC role in the pathogenesis of Alzheimer's disease. APP metabolism is also a  
 CC critical event in Alzheimer's disease pathogenesis as it leads to the  
 CC release of either toxic (Abeta) or trophic (sAPP) metabolites. Fe65 (not  
 CC defined) has been shown to interact with APP and peptides interacting  
 CC with Fe65 may also be useful in treating neurodegenerative disorders. The  
 CC compound may be capable of strengthening the interaction between the first  
 CC and the second protein. The sequence presented is the human PN7740  
 CC protein which was isolated due to its interaction with Fe65 found using  
 CC the yeast two-hybrid system  
 XX  
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206; Mismatches 0; Indels 0; Gaps 0;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60  
 DB 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIPKISLNVGCSQIGKRKKNEDRFDFAQLTDEV 120  
 DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIPKISLNVGCSQIGKRKKNEDRFDFAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHHADDSFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHHADDSFLVLTDDGI 300

QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 DB 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360

QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 6  
 ABG70826  
 ID ABG70826 standard; protein; 372 AA.  
 XX  
 AC ABG70826;  
 XX  
 DT 17-DEC-2002 (first entry)  
 XX  
 DE Fe65 interacting human protein, PN7740, protein.  
 XX  
 KW Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MK2;  
 KW mixed lineage kinase 2; ligand; transporter; cellular uptake;  
 KW neuronal death; neurodegenerative disorder; Huntington's disease;  
 KW Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS1;  
 KW PS2; Abeta; trophic; sAPP; metabolite; Fe65.  
 XX



Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60

QY 61 WDNFGIWNDRIDEPIILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120  
 DB 61 WDNFGIWNDRIDEPIILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120

QY 121 LYFAVVDGHHGPAADFCCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGPAADFCCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300

QY 301 NFWNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360  
 DB 301 NFWNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360

QY 361 FRSFASGRWA 372  
 DB 361 FRSFASGRWA 372

RESULT 8  
 AAE23976  
 ID AAE23976 standard; protein; 372 AA.  
 XX  
 AC AAE23976;  
 XX  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE Human PN7740 protein.  
 XX  
 KW Human; protein-protein interaction; neurodegenerative disorder;  
 KW Alzheimer's disease; AD; pharmaceutical; Huntington's disease;  
 KW Parkinson's disease; anticonvulsant; dementia; neuroprotective;  
 KW nootropic; PN7740.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233113-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032197.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Roch J, Bartel PL, Heichman K;  
 XX  
 DR WPI; 2002-454608/48.  
 XX  
 DR N-PSDB; AAD38691.  
 XX  
 PT New protein complex comprising Mint2 and PDE-9A proteins, useful as  
 PT targets for diagnostic tools in identifying individuals at risk for  
 PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's  
 PT disease, or dementia.  
 XX  
 PS Example 6; Page 52; 91pp; English.

CC The invention relates to the discovery of protein-protein interactions  
 CC that are involved in the pathogenesis of neurodegenerative disorders,  
 CC including Alzheimer's disease (AD). The AD interacting proteins are  
 CC useful as new targets for the identification of useful pharmaceuticals,  
 CC new targets for diagnostic tools in the identification of individuals at  
 CC risk, sequences for producing transformed cell lines, cellular models and  
 CC animal models, and new bases for therapeutic intervention in  
 CC neurodegenerative disorders, particularly AD. The DNA encoding the  
 CC protein of the invention can be used to create animals that overexpress  
 CC the protein, or animals which do not express the native gene but express  
 CC the protein. Modulators of the protein complex are useful for treating a  
 CC neurodegenerative disorder including Huntington's disease, Parkinson's  
 CC disease, dementia or Alzheimer's disease. The present sequence is human  
 CC PN7740 protein used in the exemplification of the invention  
 XX  
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60

QY 61 WDNFGIWNDRIDEPIILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120  
 DB 61 WDNFGIWNDRIDEPIILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120

QY 121 LYFAVVDGHHGPAADFCCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGPAADFCCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300

QY 301 NFWNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360  
 DB 301 NFWNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360

QY 361 FRSFASGRWA 372  
 DB 361 FRSFASGRWA 372

RESULT 9  
 AAE24078  
 ID AAE24078 standard; protein; 372 AA.  
 XX  
 AC AAE24078;  
 XX  
 DT 04-OCT-2002 (first entry)  
 XX  
 DE Human PN7740 protein.  
 XX  
 KW Protein complex; postsynaptic density protein; PSD95; Fe65; dementia;  
 KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;  
 KW PN7740; Alzheimer's disease; drug designing; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200232286-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032186.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.



PR 13-JUL-2001; 2001US-0304775P.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 XX Roch J, Bartel PL, Heichman K;  
 PI  
 XX WPI; 2002-479640/51.  
 DR N-PSDB; AAD39176.  
 XX  
 XX Novel isolated protein complex having a protein which is postsynaptic  
 PT density protein or Fe65 interacting with another protein which is PN7740  
 PT useful for drug designing for treating neurodegenerative disorder.  
 XX  
 XX Claim 24; Page 52; 102pp; English.  
 XX  
 CC The invention relates to an isolated protein complex having a first  
 CC protein which is postsynaptic density protein (PSD95) or Fe65 interacting  
 CC with a second protein which is PN7740. Protein complex of the invention  
 CC is useful for diagnosing a neurodegenerative disorder in human, for  
 CC determining a predisposition to the neuro- degenerative disorder or for  
 CC the existence of the disorder. They are used for treating degenerative  
 CC disorders such as Huntington's disease, Parkinson's disease, dementia and  
 CC Alzheimer's disease. They are also used for drug designing and for  
 CC screening compounds that modulate the interaction of proteins of the  
 CC invention. The present sequence is human PN7740 protein  
 XX  
 XX Sequence 372 AA;  
 SQ  
 Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSTAALTLVRSGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRDPDGGSGSPAT 60  
 DB 1 MSTAALTLVRSGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRDPDGGSGSPAT 60  
 QY 61 WDNFGIWDNRIDEPIILPPSIKYGKPKISLENVGCASQIGKKEKEDRDFPAQLTDEV 120  
 DB 61 WDNFGIWDNRIDEPIILPPSIKYGKPKISLENVGCASQIGKKEKEDRDFPAQLTDEV 120  
 QY 121 LYFVYDGHGPGAAADFCHTHMEKIMDLIPKKNLETLTLTFLAPLEIDKAFSSHARLSAD 180  
 DB 121 LYFVYDGHGPGAAADFCHTHMEKIMDLIPKKNLETLTLTFLAPLEIDKAFSSHARLSAD 180  
 QY 181 ATLLTSGTTATVALLRGIELVAVSGDSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRGIELVAVSGDSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 QY 241 GGFVAVNSLGQPHVNGRLAMTRSGDLDLKTSGVIAEPETKRIKLHADDPSFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRSGDLDLKTSGVIAEPETKRIKLHADDPSFLVLTDDGI 300  
 QY 301 NFVNSQEIICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAGWKYKNSEINFS 360  
 DB 301 NFVNSQEIICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAGWKYKNSEINFS 360  
 QY 361 FSRSFASSGRWA 372  
 DB 361 FSRSFASSGRWA 372  
 RESULT 10  
 AAE14451  
 ID AAE14451 standard; protein; 372 AA.  
 XX  
 AC AAE14451;  
 XX  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX Human protein phosphatase-1.  
 DE  
 XX Human; protein phosphatase; PP-1; immune system disorder; AIDS; allergy;  
 KW neurological disorder; developmental disorder; Alzheimer's disease;

KW cell proliferative disorder; Huntington's disease; arteriosclerosis;  
 KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;  
 KW leukaemia; transgenic animal; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 104. .339  
 FT Region /note= "Protein phosphatase 2C (Pp2C)"  
 FT Domain 122. .130  
 FT /label= Protein\_phosphatase\_2C\_motif  
 XX  
 PN WO200196546-A2.  
 XX  
 XX 20-DEC-2001.  
 PD  
 XX 14-JUN-2001; 2001WO-US019442.  
 PF  
 XX 16-JUN-2000; 2000US-0212447P.  
 PR 22-JUN-2000; 2000US-0213746P.  
 PR 29-JUN-2000; 2000US-0215210P.  
 PR 06-JUL-2000; 2000US-0216529P.  
 PR 12-JUL-2000; 2000US-0218080P.  
 PR 21-JUL-2000; 2000US-0220117P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;  
 PI Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;  
 PI Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;  
 PI Tribouley CM, Walia NK, Yang J, Yao MG, Yue H;  
 XX  
 DR WPI; 2002-090206/12.  
 DR N-PSDB; AAD24019.  
 XX  
 XX Novel polypeptide, useful for diagnosing, treating or preventing  
 PT disorders of growth and development, immune system, neurological and cell  
 PT proliferation diseases, comprises cancer protein phosphatase  
 PT polypeptides.  
 XX  
 PS Claim 1; Page 102-103; 116pp; English.  
 XX  
 XX The present sequence is human protein phosphatase (PP)-1. PP  
 CC polynucleotide and polypeptide are useful in the diagnosis, treatment and  
 CC prevention of immune system disorders, neurological disorders,  
 CC developmental disorders and cell proliferative disorders. Examples of  
 CC immune system disorders include acquired immune deficiency syndrome  
 CC (AIDS), severe combined immunodeficiency disease (SCID), adult  
 CC respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,  
 CC atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,  
 CC emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple  
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,  
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,  
 CC rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic  
 CC sclerosis, trauma; neurological disorders include Alzheimer's disease,  
 CC Huntington's disease, dementia, epilepsy, Parkinson's disease, mental  
 CC retardation and other developmental disorders of central nervous system  
 CC such as Down's syndrome, cerebral palsy, periodic paralysis, mental  
 CC disorders including mood, anxiety, and schizophrenic disorders, seasonal  
 CC affective disorder such as akathisia, amnesia, catatonia, dyskinesia;  
 CC developmental disorders include e.g. renal tubular acidosis, Duchenne and  
 CC Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell  
 CC proliferative disorders include e.g. actinic keratosis, arteriosclerosis,  
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer  
 CC including adenocarcinoma, leukaemia. The polypeptide and polynucleotide  
 CC are further useful for analysing proteome of a tissue or a cell type, for  
 CC screening an agonist/antagonist, a compound that specifically binds to it  
 CC or its modulator. The polynucleotide is useful for creating knockin  
 CC humanised animals (pigs) or transgenic animals (mice or rats) to model  
 CC human disease, for generating a transcript image of a tissue or cell  
 CC type, which represents the global pattern of gene expression by a  
 CC particular tissue or cell type

SQ	Sequence 372 AA;	
	Query Match 100.0%; Score 1951; DB 5; Length 372;	
	Best Local Similarity 100.0%; Pred. No. 2.8e-206;	
	Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSTAALITLVRSQGNVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
DB	1 MSTAALITLVRSQGNVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
QY	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRDFPAQLTDEV 120	
DB	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRDFPAQLTDEV 120	
QY	121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180	
DB	121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180	
QY	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
DB	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
QY	241 GGFVAMNSLQGHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHADDSEFLVLTDDGI 300	
DB	241 GGFVAMNSLQGHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHADDSEFLVLTDDGI 300	
QY	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINFS 360	
DB	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINFS 360	
QY	361 FRSFASGRWA 372	
DB	361 FRSFASGRWA 372	
RESULT 11		
ABU10309		
ID	ABU10309 standard; protein; 372 AA.	
AC	ABU10309;	
XX		
DT	07-AUG-2003 (first entry)	
XX		
DE	Human protein phosphatase SGP037.	
XX		
KW	Human; protein phosphatase; SGP037; cancer; blood; haematopoietic;	
KW	breast; colon; lung; prostate; cervical; brain; ovarian; bladder; kidney;	
KW	immune-related disease; cardiovascular disease; migraine;	
KW	neural-associated disease; nervous system disease; pain; rhinitis;	
KW	sexual dysfunction; mood disorder; attention disorder; hypotension;	
KW	cognition disorder; hypertension; psychotic disorder; dyskinesia;	
KW	neurological disorder; metabolic disorder; inflammatory disorder;	
KW	rheumatoid arthritis; chronic inflammatory bowel disease; asthma;	
KW	chronic inflammatory pelvic disease; multiple sclerosis; psoriasis;	
KW	osteoarthritis; psoriasis; atherosclerosis; autoimmune; neoplastic;	
KW	organ transplant rejection; cytostatic; neuroprotective; analgesic;	
KW	hypotensive; anticonvulsant; antiarthritic; antineumatic;	
KW	antiinflammatory; antiasthmatic; osteopathic; antipsoriatic;	
KW	antiarteriosclerotic; immunosuppressive; enzyme.	
OS	Homo sapiens.	
XX		
FN	US2003027308-A1.	
PD		
XX	06-FEB-2003.	
XX		
PE	13-NOV-2001; 2001US-00986992.	
XX		
FR	30-MAY-2000; 2000US-0208291P.	
PR	13-NOV-2000; 2000US-0246974P.	
XX		
PA	(SUGS-) SUGEN INC.	
XX		

PI	Plowman GD, Whyte D, Manning G;	
XX		
DR	WPI; 2003-466146/44.	
DR	N-PSDB; ABX95873.	
XX		
PT	New isolated, enriched or purified nucleic acid molecule encoding a	
PT	phosphatase polypeptide, useful for treating diseases, e.g. cancers, or	
PT	immune-related cardiovascular, brain and neuronal, metabolic or	
PT	inflammatory disorders.	
XX		
PS	Claim 1; Fig 2; 45pp; English.	
XX		
CC	The present invention relates to the isolation of a novel human protein	
CC	phosphatase designated SGP037, and the polynucleotide sequence encoding	
CC	it. The gene encoding human SGP037 maps to chromosome 4q21. The SGP037	
CC	polypeptide and the polynucleotide sequence encoding it are useful for	
CC	treating diseases or disorders such as cancers (e.g. cancer of the blood	
CC	or haematopoietic origin, breast, colon, lung, prostate, cervical, brain,	
CC	ovarian, bladder or kidney), immune-related diseases and disorders,	
CC	cardiovascular diseases, brain and neuronal-associated diseases (e.g.	
CC	central or peripheral nervous system diseases, migraines, pain, sexual	
CC	dysfunction, mood disorders, attention disorders, cognition disorders,	
CC	hypotension, hypertension, psychotic disorders, neurological disorders or	
CC	dyskinesias), metabolic disorders, and inflammatory disorders (e.g.	
CC	rheumatoid arthritis, chronic inflammatory bowel disease, chronic	
CC	inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,	
CC	psoriasis, atherosclerosis, rhinitis, autoimmunity or organ transplant	
CC	rejection). The present sequence represents human SGP037	
XX		
SQ	Sequence 372 AA;	
	Query Match 100.0%; Score 1951; DB 6; Length 372;	
	Best Local Similarity 100.0%; Pred. No. 2.8e-206;	
	Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSTAALITLVRSQGNVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
DB	1 MSTAALITLVRSQGNVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
QY	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRDFPAQLTDEV 120	
DB	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRDFPAQLTDEV 120	
QY	121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180	
DB	121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180	
QY	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
DB	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
QY	241 GGFVAMNSLQGHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHADDSEFLVLTDDGI 300	
DB	241 GGFVAMNSLQGHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHADDSEFLVLTDDGI 300	
QY	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINFS 360	
DB	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINFS 360	
QY	361 FRSFASGRWA 372	
DB	361 FRSFASGRWA 372	
RESULT 12		
AAO23055		
ID	AAO23055 standard; protein; 372 AA.	
XX		
AC	AAO23055;	
XX		
DT	17-SEP-2003 (first entry)	
XX		
DE	Human serine/threonine PP2C phosphatase SGP037 protein.	

XX Cytostatic; immunosuppressive; cardiovascular; hypotensive; hypertensive; antinigraine; analgesic; nootropic; tranquilizer; antirheumatic; brain; antiarthritic; antiinflammatory; gynaecological; neuroprotective; ocular; antiasthmatic; osteopathic; antipsoriatic; antiarteriosclerotic; obesity; antiatheric; serine threonine phosphatase; STP; PP2C; cancer; immune; cardiovascular disease; neuronal; sexual dysfunction; migraine; glaucoma; psychotic; neurological; schizophrenia; metabolic; inflammatory; SGP037; multiple sclerosis; viral infection; HIV; transgenic; gene therapy; enzyme; human; chromosome 4q21.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 104..339

XX /note= "Catalytic region"

XX WO2003042390-A1.

XX 22-MAY-2003.

XX 13-NOV-2001; 2001WO-US043063.

XX 13-NOV-2001; 2001WO-US043063.

XX (FLOW/) PLOWMAN G D.

XX Plowman GD, Manning G, Whyte D;

XX WPI; 2003-449576/42.

XX N-PSDB; AAL55773.

XX New phosphatase nucleic acid molecule and polypeptide, useful for diagnosing or treating phosphatase-related disorders such as cancers, immune-related disorders, cardiovascular disease, and inflammatory disorders.

XX Claim 26; Fig 2; 152pp; English.

XX The invention relates to a novel isolated nucleic acid molecule encoding a serine/threonine phosphatase (STP) polypeptide which is a member of the PP2C family. PP2C phosphatases are involved in a number of cellular processes including modulation of integrin signal transduction and regulation of the TAK1 signalling pathway, cellular channels, cyclin dependent kinases and the Ras pathway. The methods and compositions of the present invention may be useful during the diagnosis or treatment of a variety of disorders including cancers, immune-related and cardiovascular disease, brain or neuronal-associated diseases such as e.g. schizophrenia and migraine, psychotic and neurological disorders e.g. schizophrenia and metabolic disorders such as obesity. Furthermore, ocular disease, such as glaucoma and inflammatory disorders e.g. multiple sclerosis may be addressed, as well as viral infections caused by HIV and other pathological agents. Finally, the molecules of the invention may be utilised in the production of transgenic animals and during gene therapy.

XX The current sequence is that of the human serine/threonine PP2C phosphatase SGP037 protein of the invention

XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 6; Length 372;

Best Local Similarity 100.0%; Pred. No. 2.8e-206;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLIQDDRVTPTCHSSTSPRCSFDPDGGSPAT 60

Db 1 MSTAALITLVRSQGNQVRRVLLSSRLIQDDRVTPTCHSSTSPRCSFDPDGGSPAT 60

Qy 61 WDNFGIWDNRIDEIPILLPPSIKYCKPIKISLVNVCASQIGKKEKNEDEDFDQLTDEV 120

Db 61 WDNFGIWDNRIDEIPILLPPSIKYCKPIKISLVNVCASQIGKKEKNEDEDFDQLTDEV 120

Qy 121 LYFVAVYDGHGPPAAADFCHTHMEKCIIMDLLPKKNLETLTLTFLAFLDKAFSSHARLSAD 180

Db 121 LYFVAVYDGHGPPAAADFCHTHMEKCIIMDLLPKKNLETLTLTFLAFLDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240

Db 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240

Qy 241 GGFVAVNSLGQPHVNGRLAMWRSIGDLDKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300

Db 241 GGFVAVNSLGQPHVNGRLAMWRSIGDLDKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300

Qy 301 NFMVNSQETCDFVNOCHDNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

Db 301 NFMVNSQETCDFVNOCHDNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

Qy 361 FRSFPASSGRWA 372

Db 361 FRSFPASSGRWA 372

RESULT 13

ADB66824

ID ADB66824 standard; protein; 372 AA.

XX ADB66824;

XX 04-DEC-2003 (first entry)

XX Human PN7740.

XX human; drug candidate screening; neurodegenerative disorder;

XX Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease.

XX Homo sapiens.

XX US2002115119-A1.

XX 22-AUG-2002.

XX 10-OCT-2001; 2001US-00973063.

XX 17-OCT-2000; 2000US-0240790P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Roch J, Bartel PL, Heichman K;

XX WPI; 2003-719962/68.

XX N-PSDB; ADB66827.

XX Screening drug candidates for modulating interaction of complexes of protein, by combining protein in the presence or absence of a drug to form first and second complex, and measuring and comparing both the complexes.

XX Example 2; Page 22; 36pp; English.

XX The invention relates to a method of screening drug candidates for modulating interaction of proteins in a complex. The method is useful for screening drug candidates useful in treating neurodegenerative disorder, by measuring the activity of a protein selected from Mint2 and PDE-9A in the presence or absence of the drug, and comparing the activity measured, where if there is a difference in activity, then the drug is a drug candidate for treating the neurodegenerative disorder. The

XX neurodegenerative disorder is Huntington's disease, Parkinson's disease, dementia, or Alzheimer's disease, preferably Alzheimer's disease. The drug, modulator or compound identified by the methods of the invention are useful for treating a neurodegenerative disorder. The present sequence represents the amino acid sequence of human PN7740.

XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 7; Length 372;

Best Local Similarity 100.0%; Pred. No. 2.8e-206;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 |||||  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 |||||

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120  
 |||||  
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120  
 |||||

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180  
 |||||  
 DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180  
 |||||

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 |||||  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 |||||

QY 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 |||||  
 DB 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 |||||

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 |||||  
 DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 |||||

QY 361 FSRSPASSGRWA 372  
 |||||  
 DB 361 FSRSPASSGRWA 372  
 |||||

RESULT 14  
 ADD73452  
 ID ADD73452 standard; protein; 372 AA.  
 XX  
 AC ADD73452;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Novel human protein PN7740.  
 XX  
 KW neotropic; neuroprotective; antiparkinsonian; protein binding modulator;  
 KW drug screening; neurodegenerative disorder; Huntington's Disease;  
 KW Parkinson's Disease; dementia; Alzheimer's Disease; AD; APP; presenilin;  
 KW protein-protein interaction; drug target identification; human;  
 KW yeast two-hybrid assay; PN7740.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003186317-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 09-OCT-2001; 2001US-00971782.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Roch J, Bartel PL, Heichman K;  
 XX  
 DR WPI; 2003-852417/79.  
 DR N-PSDB; ADD73455.  
 XX

In vitro screening for drug useful for treating neurodegenerative  
 PT disorder, e.g. Alzheimer's Disease, involves comparing the amount of two  
 PT complexes formed from combined proteins of protein complex in the  
 PT presence and absence of drug.  
 XX  
 XX Example 2-33; SEQ ID NO 4; 36pp; English.  
 PS The invention describes screening a drug in vitro by combining proteins  
 CC of a protein complex in the presence of a drug to form a first complex;  
 CC

CC combining the proteins in the absence of the drug to form a second  
 CC complex, measuring the amount of the two complexes; and comparing the  
 CC amount of the first complex with the amount of the second complex. The  
 CC method is useful for screening drug candidates capable of modulating the  
 CC interaction of the proteins of a protein complex, useful for treating a  
 CC neurodegenerative disorder, e.g. Huntington's Disease, Parkinson's  
 CC Disease, dementia or Alzheimer's Disease (AD). The inventive method  
 CC provides for the discovery of additional proteins interacting with  
 CC various domains of the major Alzheimer proteins, including APP and the  
 CC presenilins. It can also identify the protein-protein interactions that  
 CC are involved in Alzheimer's Disease (AD) pathogenesis, and to identify  
 CC drug targets. This is the amino acid sequence of a novel human protein  
 CC PN7740 identified using yeast two-hybrid assay with a human brain bait  
 CC protein.  
 XX  
 SQ Sequence 372 AA;  
 Query Match 100.0%; Score 1951; DB 7; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 |||||  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 |||||

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120  
 |||||  
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120  
 |||||

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180  
 |||||  
 DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180  
 |||||

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 |||||  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 |||||

QY 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 |||||  
 DB 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 |||||

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 |||||  
 DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 |||||

QY 361 FSRSPASSGRWA 372  
 |||||  
 DB 361 FSRSPASSGRWA 372  
 |||||

RESULT 15  
 ADQ14718  
 ID ADQ14718 standard; protein; 372 AA.  
 XX  
 AC ADQ14718;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human protein phosphatase SGP037.  
 XX  
 KW Human; enzyme; protein phosphatase; SGP037; chromosome 4q21;  
 KW acute lymphoblastic leukaemia; cancer; immune-related disease;  
 KW cardiovascular disease; brain disease; neuronal-associated disease;  
 KW metabolic disorder; inflammatory disorder; rheumatoid arthritis;  
 KW chronic inflammatory bowel disease; chronic inflammatory pelvis disease;  
 KW multiple sclerosis; asthma; osteoarthritis; psoriasis; atherosclerosis;  
 KW rhinitis; autoimmunity; organ transplant rejection;  
 KW central nervous system disease; migraine; pain; sexual dysfunction;  
 KW mood disorder; attention disorder; cognition disorder; hypotension;  
 KW hypertension; psychotic disorder; neurological disorder; dyskinesia.  
 XX  
 OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
FT Domain 12..301  
FT /label = pPC2  
FT /note= "phosphatase domain"  
FT Domain 104..339  
FT /label = pPC2  
FT /note= "phosphatase domain"

US2004132155-A1.

XX 08-JUL-2004.

XX 20-NOV-2003; 2003US-00716488.

XX 30-MAY-2000; 2000US-0208291P.

XX 13-NOV-2000; 2000US-0246974P.

XX 30-MAY-2001; 2001US-00866987.

XX 13-NOV-2001; 2001US-00986992.

XX (SUGE-) SUGEN INC.

XX Plowman GD, Whyte D, Manning G;

XX WPI; 2004-517014/49.

XX New nucleic acid molecule encoding a phosphatase polypeptide, useful in  
XX diagnosing and treating cancers, cardiovascular disease, inflammatory  
XX disorders, central or nervous system diseases, pain, cognition disorders,  
XX or dyskinesias.

XX Claim 1; SEQ ID NO 2; 47pp; English.

XX The invention relates to an isolated, enriched or purified nucleic acid  
XX molecule encoding a phosphatase polypeptide, the phosphatase being the  
XX protein phosphatase SGP037 whose sequence appears as ADQ14718. Also are  
XX an isolated, enriched or purified phosphatase polypeptide (comprising an  
XX amino acid sequence at least 90% identical to ADQ14718 or an amino acid  
XX sequence of ADQ14718, except that the polypeptide lacks one or more, but  
XX not all, of an N-terminal domain, a C terminal catalytic domain, a  
XX catalytic domain, a C-terminal domain, a coiled-coil structure region, a  
XX proline rich region, a spacer region, and a C-terminal tail), an antibody  
XX or antibody fragment having specific binding affinity to the phosphatase  
XX polypeptide (or to a domain of the polypeptide), a hybridoma which  
XX produces the antibody, a kit comprising the antibody (and a negative  
XX control antibody), identifying a substance that modulates the activity of  
XX a phosphatase polypeptide, identifying a substance that modulates the  
XX activity of a phosphatase polypeptide in a cell, treating a disease or  
XX disorder, detecting a phosphatase polypeptide in a sample as a diagnostic  
XX tool for a disease or disorder, a recombinant cell comprising the nucleic  
XX acid and a vector comprising the nucleic acid. The nucleic acid molecule  
XX and the encoded polypeptide, methods and composition are useful in  
XX diagnosing and treating cancers (e.g. cancer of tissues, blood or  
XX haematopoietic origin, breast, colon, lung prostate, cervical, brain  
XX ovarian, bladder, or kidney), immune-related diseases and disorders,  
XX cardiovascular disease, brain or neuronal-associated diseases, metabolic  
XX disorders, inflammatory disorders (e.g. rheumatoid arthritis, chronic  
XX inflammatory bowel disease, chronic inflammatory pelvis disease, multiple  
XX sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis,  
XX autoimmunity, or organ transplant rejection), central or nervous system  
XX diseases, migraines, pain, sexual dysfunction, mood disorders, attention  
XX disorders, cognition disorders, hypertension, mood disorders, psychotic  
XX disorders, neurological disorders, or dyskinesias. The gene for SGP037 is  
XX located on chromosome 4q21 (a region associated with acute lymphoblastic  
XX anaemia). The present sequence is the SGP037 protein.

XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 8; Length 372;  
Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAAALITLVRSGNQVRRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSGPAT 60  
|||||

Db 1 MSTAAALITLVRSGNQVRRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSGPAT 60  
QY 61 WDNFGIWDNRIDRPIILLPPSIKYGKPIPKISLNVGSCASQIGKRKENEDRDFPAQLTDEV 120  
|||  
Db 61 WDNFGIWDNRIDRPIILLPPSIKYGKPIPKISLNVGSCASQIGKRKENEDRDFPAQLTDEV 120  
|||  
QY 121 LYFAVYDGHGGPAAADFCCHTHMEKICMDLLPKKKNLETLTLTFLAFLETDKAFSSHARLSAD 180  
|||  
Db 121 LYFAVYDGHGGPAAADFCCHTHMEKICMDLLPKKKNLETLTLTFLAFLETDKAFSSHARLSAD 180  
|||  
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSPAILCRKGKPMKLTIDHTPERKDEKERIKKC 240  
|||  
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSPAILCRKGKPMKLTIDHTPERKDEKERIKKC 240  
|||  
QY 241 GGFVAVNSLQCPHVNGRLAMTRISIGDLDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300  
|||  
Db 241 GGFVAVNSLQCPHVNGRLAMTRISIGDLDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300  
|||  
QY 301 NFMVNSQEICDFVYNQCHDPNEAAHAHVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
|||  
Db 301 NFMVNSQEICDFVYNQCHDPNEAAHAHVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
|||  
QY 361 FRSRSPASSGRWA 372  
|||  
Db 361 FRSRSPASSGRWA 372  
|||

Search completed: June 17, 2005, 00:54:10  
Job time : 168 secs

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